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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 11:45:41 : Search time 2813 Seconds
(without alignments)
6758.073 Million cell updates/sec

Title: US-10-724-225-1_COPY_1_402

Perfect score: 402
Sequence: 1 ATGCGAATACCAACATGTC.....ACCTTGAAGTGGAGATGAT 402

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: *
1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_on: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pt: *
10: gb_ro: *
11: gb_sbs: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 402 | 100.0 | 646 | 9 AF385323 | AF385323 Homo sapi |
| 2 | 402 | 100.0 | 652 | 6 AR207094 | AR207094 Sequence |
| 3 | 402 | 100.0 | 659 | 9 HSA491698 | AJ491698 Homo sapi |
| 4 | 402 | 100.0 | 729 | 6 A61763 | A61763 Sequence 3 |
| 5 | 402 | 100.0 | 729 | 6 AR264886 | AR264886 Sequence |
| 6 | 402 | 100.0 | 732 | 9 HSA430612 | AJ430612 Homo sapi |
| 7 | 402 | 100.0 | 852 | 6 A44504 | A44504 Sequence 4 |
| 8 | 402 | 100.0 | 1476 | 6 A61359 | A61359 Sequence 1 |
| 9 | 402 | 100.0 | 1476 | 6 AX057138 | AX057138 Sequence |
| 10 | 402 | 100.0 | 1476 | 6 AX695559 | AX695559 Sequence |
| 11 | 402 | 100.0 | 1476 | 9 BT007258 | BT007258 Homo sapi |
| 12 | 402 | 100.0 | 1476 | 12 BT007935 | BT007935 Synthetic |
| 13 | 402 | 100.0 | 2372 | 6 CO717844 | CO717844 Sequence |
| 14 | 402 | 100.0 | 2372 | 6 AR000256 | AR000256 Sequence |
| 15 | 402 | 100.0 | 2372 | 6 AR009781 | AR009781 Sequence |
| 16 | 402 | 100.0 | 2372 | 6 AR028963 | AR028963 Sequence |
| 17 | 402 | 100.0 | 2372 | 6 AR154584 | AR154584 Sequence |
| 18 | 402 | 100.0 | 2372 | 6 BD233925 | BD233925 Method an |
| 19 | 402 | 100.0 | 2372 | 6 I11727 | I11727 Sequence 1 |

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| 21 | 402 | 100.0 | 2372 | 6 I21256 | I21256 Sequence 1 |
| 22 | 402 | 100.0 | 2372 | 6 I25341 | I25341 Sequence 2 |
| 23 | 402 | 100.0 | 2372 | 6 I36472 | I36472 Sequence 2 |
| 24 | 402 | 100.0 | 2372 | 6 I40222 | I40222 Sequence 2 |
| 25 | 402 | 100.0 | 2372 | 6 I79856 | I79856 Sequence 2 |
| 26 | 402 | 100.0 | 2372 | 6 I86850 | I86850 Sequence 2 |
| 27 | 402 | 100.0 | 2372 | 6 AR212312 | AR212312 Sequence |
| 28 | 402 | 100.0 | 2372 | 6 AR214399 | AR214399 Sequence |
| 29 | 402 | 100.0 | 2372 | 6 AX328941 | AX328941 Sequence |
| 30 | 402 | 100.0 | 2372 | 6 AX587651 | AX587651 Sequence |
| 31 | 402 | 100.0 | 2372 | 6 AX695558 | AX695558 Sequence |
| 32 | 402 | 100.0 | 2372 | 6 BD073962 | BD073962 Antisense |
| 33 | 402 | 100.0 | 2372 | 6 BD138075 | BD138075 Antisense |
| 34 | 402 | 100.0 | 2372 | 9 HSP53AS6G | Z12020 H. sapiens m |
| 35 | 402 | 100.0 | 2372 | 9 HUMS552A | M92424 Human p53-a |
| 36 | 402 | 100.0 | 3121 | 9 BC067077 | BC067077 Homo sapi |
| 37 | 360.4 | 89.7 | 1460 | 4 AF100705 | AF100705 Canis fam |
| 38 | 358.8 | 89.3 | 1469 | 4 AB031276 | AB031276 Canis fam |
| 39 | 358.8 | 88.9 | 1477 | 4 AF322416 | AF322416 Canis fam |
| 40 | 357.2 | 88.9 | 2042 | 4 AB099709 | AB099709 Felis cat |
| 41 | 355.6 | 88.5 | 1476 | 4 AF121140 | AF121140 Equus cab |
| 42 | 342 | 85.1 | 1361 | 9 AF092844 | AF092844 Homo sapi |
| 43 | 327.4 | 81.4 | 388 | 9 AF092843 | AF092843 Homo sapi |
| 44 | 289.2 | 71.9 | 1470 | 6 AX695556 | AX695556 Sequence |
| 45 | 289.2 | 71.9 | 1470 | 10 MMU47934 | U47934 Mus musculu |

ALIGNMENTS

RESULT 1

AF385323

LOCUS AF385323 646 bp mRNA linear PRI 11-OCT-2001
DEFINITION Homo sapiens MDM2 variant FB26 (MDM2) mRNA, complete cds,
alternatively spliced.

ACCESSION AF385323

AF385323.1 GI:16033442

VERSION AF385323.1

GI:16033442

KEYWORDS

ORGANISM

REFERENCE

1 (bases 1 to 646)

AUTHORS

Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.

TITLE

Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma

JOURNAL

2 (bases 1 to 646)

REFERENCE

Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.

AUTHORS

Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's

TITLE

Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA

JOURNAL

Location/Qualifiers

FEATURES

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source

1..646

CDs

1..588

gene

1..646

ORIGIN

1..646

REFERENCE

1 (bases 1 to 646)

AUTHORS

Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.

TITLE

Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma

JOURNAL

2 (bases 1 to 646)

Query Match 100.0%; Score 402; DB 9; Length 646;
 Best Local Similarity 100.0%; Pred. No. 2.4e-93;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGCTGTGTAACCTAGTGTGCTGTAAACCTACACAGATTCCA 60
 DB 1 ATGTGCAATACCAACATGCTGTGTAACCTAGTGTGCTGTAAACCTACACAGATTCCA 60

QY 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120
 DB 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120

QY 121 GTTGTCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGCCAGTAT 180
 DB 121 GTTGTCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGCCAGTAT 180

QY 181 ATTATGACTAAAGCATTTATGATGAGACACACATATTTGTTCAATGAT 240
 DB 181 ATTATGACTAAAGCATTTATGATGAGACACACATATTTGTTCAATGAT 240

QY 241 CTCTAGAGATTGTTGGTGCCAAAGCTCTCTGTGAAAGACAGAAAATATAT 300
 DB 241 CTCTAGAGATTGTTGGTGCCAAAGCTCTCTGTGAAAGACAGAAAATATAT 300

QY 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGAAATCATCGACTCAGTACA 360
 DB 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGAAATCATCGACTCAGTACA 360

QY 361 TCTGTAGTGAAGAAGAGGTGTACCTTTGAAGGTGGAAGTAT 402
 DB 361 TCTGTAGTGAAGAAGAGGTGTACCTTTGAAGGTGGAAGTAT 402

RESULT 2
 LOCUS AR207094
 DEFINITION Sequence 3 from patent US 6372490.
 ACCESSION AR207094
 VERSION AR207094.1 GI:21505896
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 652)
 AUTHORS Mandabalan, K., Yang, M. and Schulz, V.
 TITLE Nucleic acid encoding the MDW interacting protein
 JOURNAL Patent: US 6372490-A 3 16-Apr-2002;
 FEATURES
 source 1..652
 location/Qualifiers
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 /mol_type="unassigned DNA"

ORIGIN
 Query Match 100.0%; Score 402; DB 6; Length 652;
 Best Local Similarity 100.0%; Pred. No. 2.4e-93;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGCTGTGTAACCTAGTGTGCTGTAAACCTACACAGATTCCA 60
 DB 1 ATGTGCAATACCAACATGCTGTGTAACCTAGTGTGCTGTAAACCTACACAGATTCCA 60

QY 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120
 DB 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120

QY 121 GTTGTCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGCCAGTAT 180
 DB 121 GTTGTCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGCCAGTAT 180

QY 181 ATTATGACTAAAGCATTTATGATGAGACACACATATTTGTTCAATGAT 240
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QY 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGAAATCATCGACTCAGTACA 360
 DB 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGAAATCATCGACTCAGTACA 360

QY 361 TCTGTAGTGAAGAAGAGGTGTACCTTTGAAGGTGGAAGTAT 402
 DB 361 TCTGTAGTGAAGAAGAGGTGTACCTTTGAAGGTGGAAGTAT 402

RESULT 3
 LOCUS HSA491698
 DEFINITION Homo sapiens mRNA for p53-binding protein alternatively spliced isoform HB67 (MDM2 gene).
 ACCESSION AJ491698
 VERSION AJ491698.1 GI:21628666
 KEYWORDS alternative splicing; MDM2 gene; p53-binding protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Bartel, F., Pinkert, D., Kappler, M., Bache, M., Schmidt, H. and Taubert, H.
 TITLE Alternatively and aberrantly spliced transcripts of the MDM2 mRNA occur frequently in human soft tissue sarcoma and in multiple normal tissues
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 659)
 AUTHORS Bartel, F.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2002) Bartel F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097 Halle, GERMANY
 FEATURES
 source 1..659
 location/Qualifiers
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 /gene="MDM2"
 1..501
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 /db_xref="GI:21628667"
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ORIGIN
 Query Match 100.0%; Score 402; DB 9; Length 659;
 Best Local Similarity 100.0%; Pred. No. 2.4e-93;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGCTGTGTAACCTAGTGTGCTGTAAACCTACACAGATTCCA 60
 DB 1 ATGTGCAATACCAACATGCTGTGTAACCTAGTGTGCTGTAAACCTACACAGATTCCA 60

QY 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120
 DB 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120

QY 121 GTTGTGCACAAAAGACATTATATGAGAGGCTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGTGCACAAAAGACATTATATGAGAGGCTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 240
DB 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 240
QY 241 CTCTTAGAGATTTGTTGGCGGCCAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
DB 241 CTCTTAGAGATTTGTTGGCGGCCAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 360
DB 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 360
QY 361 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGTAT 402
DB 361 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGTAT 402

RESULT 4
LOCUS A61763 729 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 3 from Patent WO9711367.
ACCESSION A61763
VERSION A61763.1 GI:3715951
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1
AUTHORS Chene, P. and Hochkeppel, H.
TITLE ASSAY FOR IDENTIFYING INHIBITORS OF THE INTERACTION BETWEEN PROTEINS p53 AND dm2
JOURNAL Patent: WO 9711367-A 3 27-MAR-1997;
FEATURES CIBA GEIGY AG (CH)
source location/Qualifiers
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/db_xref="taxon:32644"
84..650
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/protein_id="CAA03593.1"
/db_xref="GI:3715952"
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ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 60
DB 84 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 143
QY 61 GCTTCGGAACAAGAGACCTGTGTAGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 144 GCTTCGGAACAAGAGACCTGTGTAGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 203
QY 121 GTTGTGACAAAAGACACTTATATGATGAGAGAGGTTCTTTTATCTTGGCAGATAT 180
DB 204 GTTGTGACAAAAGACACTTATATGATGAGAGAGGTTCTTTTATCTTGGCAGATAT 263
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 240
DB 264 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 323

QY 241 CTCTAGAGATTTGTTGGCGGCCAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
DB 324 CTCTAGAGATTTGTTGGCGGCCAGCTTCTCTGTGAAGAGCAGAGAAATATAT 383
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 360
DB 384 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 443
QY 361 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGTAT 402
DB 444 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGTAT 485

RESULT 5
LOCUS AR264886 729 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6492116.
ACCESSION AR264886
VERSION AR264886.1 GI:29693255
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 729)
AUTHORS Chene, P. and Hochkeppel, H.-K.
TITLE Assay for identifying inhibitors of the interaction between proteins p53 and dm2
JOURNAL Patent: US 6492116-A 3 10-DEC-2002;
FEATURES location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 60
DB 84 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 143
QY 61 GCTTCGGAACAAGAGACCTGTGTAGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 144 GCTTCGGAACAAGAGACCTGTGTAGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 203
QY 121 GTTGTGACAAAAGACACTTATATGATGAGAGAGGTTCTTTTATCTTGGCAGATAT 180
DB 204 GTTGTGACAAAAGACACTTATATGATGAGAGAGGTTCTTTTATCTTGGCAGATAT 263
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 240
DB 264 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 323
QY 241 CTCTAGAGATTTGTTGGCGGCCAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
DB 324 CTCTAGAGATTTGTTGGCGGCCAGCTTCTCTGTGAAGAGCAGAGAAATATAT 383
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 360
DB 384 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 443
QY 361 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGTAT 402
DB 444 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGTAT 485

RESULT 6
LOCUS HSA430612 732 bp mRNA linear PRI 15-FEB-2002
DEFINITION Homo sapiens mRNA for MDM2 isoform KB9.
ACCESSION AJ430612

VERSION AJ430612.1 GI:18698329
KEYWORDS lymphocytes; MDM2 isoform KB9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Bartel, F., Pinkert, D., Kappler, M., Bache, M., Schmidt, H. and Taubert, H.
TITLE Alternatively and Aberrantly Spliced Transcripts of the MDM2-mRNA Occur Frequently in Human Soft Tissue Sarcomas and in Multiple Normal Tissues
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 732)
REFERENCE Bartel, F.
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2002) Bartel F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097 Halle, GERMANY

FEATURES
source location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1..732
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/codon_start=1
/evidence=experimental
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/db_xref="GI:18698330"
/db_xref="tRMBL:Q8TE47"
/translation="MCTNMSVPTDGVTTTSQIPASRQETLVKPKLLKLSVGAQ KDTYMKELVPIYQYIMTKRLIDKQKHLYVCSNDLJGDFGVPSVSEHKIYTM IYRNLVVNQESSDSGTSVENRCHLEGSDDQIVQLEQEKPSSSHVSPTS RRRAISRETEODKEBSVESLPLNAIEPCVICOGRKNCIYHGKTHIMACFTCAK KLRKNRPFVCHQPIQIMVITYFP"

ORIGIN
Query Match 100.0%; Score 402; DB 9; Length 732;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAATACCAATGCTGTGACCTAGTGTGCTTGAACCTACCAAGATTCCA 60
DB 1 ATGCGAATACCAATGCTGTGACCTAGTGTGCTTGAACCTACCAAGATTCCA 60
QY 61 GCTTCGGAACAAGAGACCTGCTGAGCAACAAGCATTGCTTTGAAGTTAAAGTCT 120
DB 61 GCTTCGGAACAAGAGACCTGCTGAGCAACAAGCATTGCTTTGAAGTTAAAGTCT 120
QY 121 GTTGTGACAAAAAAGACATTATATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
DB 121 GTTGTGACAAAAAAGACATTATATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
QY 181 ATTATGACTAAAGATTATATGATGAGAGCAACAATATGTTGTTCAAAATGAT 240
DB 181 ATTATGACTAAAGATTATATGATGAGAGCAACAATATGTTGTTCAAAATGAT 240
QY 241 CTTCTAGAGATTGTTGCGCGTGCAGAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
DB 241 CTTCTAGAGATTGTTGCGCGTGCAGAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
QY 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGAGAAATATGATGATGATGAT 360
DB 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGAGAAATATGATGATGATGAT 360
QY 361 TCTGTAGTGAAGAACAGGTGTCACTTTGAAGGTGGAGTAT 402
DB 361 TCTGTAGTGAAGAACAGGTGTCACTTTGAAGGTGGAGTAT 402

RESULT 7
LOCUS A44504 852 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 4 from Patent WO9514233.
ACCESSION A44504
VERSION A44504.1 GI:2299322
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 852)
AUTHORS Zentgraf, H., Klein, R., Frey, M. and Martens, R.
TITLE METHOD OF IDENTIFYING HDM-2-SPECIFIC ANTIBODIES
JOURNAL Patent: WO 9514233-A 4 26-MAY-1995;
DEUTSCHES KREBSFORSCH (DE)
COMMENT Other publication DE 4339533 950614
Other publication DE 4345249 950524.
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 852;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAATACCAATGCTGTGACCTAGTGTGCTTGAACCTACCAAGATTCCA 60
DB 1 ATGCGAATACCAATGCTGTGACCTAGTGTGCTTGAACCTACCAAGATTCCA 60
QY 61 GCTTCGGAACAAGAGACCTGCTGAGCAACAAGCATTGCTTTGAAGTTAAAGTCT 120
DB 61 GCTTCGGAACAAGAGACCTGCTGAGCAACAAGCATTGCTTTGAAGTTAAAGTCT 120
QY 121 GTTGTGACAAAAAAGACATTATATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
DB 121 GTTGTGACAAAAAAGACATTATATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
QY 181 ATTATGACTAAAGATTATATGATGAGAGCAACAATATGTTGTTCAAAATGAT 240
DB 181 ATTATGACTAAAGATTATATGATGAGAGCAACAATATGTTGTTCAAAATGAT 240
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DB 241 CTTCTAGAGATTGTTGCGCGTGCAGAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
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QY 361 TCTGTAGTGAAGAACAGGTGTCACTTTGAAGGTGGAGTAT 402
DB 361 TCTGTAGTGAAGAACAGGTGTCACTTTGAAGGTGGAGTAT 402

RESULT 8
LOCUS A61359 1476 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 1 from Patent WO9709343.
ACCESSION A61359
VERSION A61359.1 GI:3715769
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Tocque, B., Dubs-Potterzman, M. and Maslyk, B.
TITLE ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF CANCERS
JOURNAL Patent: WO 9709343-A 1 13-MAR-1997;

COMMENT RHONE POULENC RORER SA (FR)
Other publication FR 2738151 970307.
FEATURES location/Qualifiers

SOURCE

CDS

1..1476
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/db_xref="GI:3715770"
/translation="MCNTNMSVPPDGAVTTTSQIPASROETLVPRKPLLKLLKSVGAQ
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GKDKGEISEKAKLENSTQAEEDVPDCKKITVNDRESCEVEEDDKITQASQOSEB
DYQSPSTSSSIIVSSQEDVFEFEETQDESEVSSSLPINALIEPCVICOGRPNKGI
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ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTCGAATACCAACATGTCTGTACCTTATGATGCTGTAAACCACTTCACAGATTCCA 60
Db 1 ATGTCGAATACCAACATGTCTGTACCTTATGATGCTGTAAACCACTTCACAGATTCCA 60
Oy 61 GCTTCGGAACAAGAGACCCCTGTGAGCAAGGCATTGCTTTGAAGTTATTAAGTCT 120
Db 61 GCTTCGGAACAAGAGACCCCTGTGAGCAAGGCATTGCTTTGAAGTTATTAAGTCT 120
Oy 121 GTTGTCACAAAAAGACACTTATATGATGAGCAAGGTTCTTTTATCTTGCCAGATAT 180
Db 121 GTTGTCACAAAAAGACACTTATATGATGAGCAAGGTTCTTTTATCTTGCCAGATAT 180
Oy 181 ATTATGACTAAACGATTATATGATGAGCAACATATTTGTAATTTGTTCAATGAT 240
Db 181 ATTATGACTAAACGATTATATGATGAGCAACATATTTGTAATTTGTTCAATGAT 240
Oy 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGGAAGAGCACAAGAAATATAT 300
Db 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGGAAGAGCACAAGAAATATAT 300
Oy 301 ACCATGATCTACAGAACTTGTAGTATGATCAATCAGCAGAAATATCGACTCAGTACA 360
Db 301 ACCATGATCTACAGAACTTGTAGTATGATCAATCAGCAGAAATATCGACTCAGTACA 360
Oy 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGGTGGAGTAT 402
Db 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGGTGGAGTAT 402

RESULT 9
AX057138 1476 bp DNA linear PAT 17-JAN-2001
LOCUS AX057138
DEFINITION Sequence 14 from Patent WO0075184.
ACCESSION AX057138
VERSION AX057138.1 GI:12309959
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Zhang, H., Tsvelkov, L.M., and Kondo, T.
AUTHORS Modulation of protein levels using the scf complex
TITLE Patent: WO 0075184-A 14 14-DEC-2000;
JOURNAL VALE UNIVERSITY (US)
FEATURES location/Qualifiers

source

CDS

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1..1476
/note="unnamed protein product; Human MDK2"
/codon_start=1
/protein_id="CAC22426.1"
/db_xref="GI:12309960"
/translation="MCNTNMSVPPDGAVTTTSQIPASROETLVPRKPLLKLLKSVGAQ
KDTYTMKEVLFYLGQYIMTRKLYDEKQOHVYGCNDLGLDFGVPSFVSEHRTIYM
IYRNLVYVNOESDSESGTSENRCHLEGSQDQDLVQELQOEKPSSSHVSRSTSS
RRRAISTEENSDELSEGRORKHKSISLSFDESLALCVIREICCRSSSESTGT
PSNPDLAGVSEHSGMDLDDSVSDQSVSEFVSLSESDYSLSEGOEISDEDEYV
QVTVYQAGESTDSFEEDPEISLADYKCTSCNENPPLPSHCNRCWALRENNMLPEBK
GKDKGEISEKAKLENSTQAEEDVPDCKKITVNDRESCEVEEDDKITQASQOSEB
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VHGKTHLMACFTCAKCLKKRNKPCVPCROPIDQIVLTYPF"

ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTCGAATACCAACATGTCTGTACCTTATGATGCTGTAAACCACTTCACAGATTCCA 60
Db 1 ATGTCGAATACCAACATGTCTGTACCTTATGATGCTGTAAACCACTTCACAGATTCCA 60
Oy 61 GCTTCGGAACAAGAGACCCCTGTGAGCAAGGCATTGCTTTGAAGTTATTAAGTCT 120
Db 61 GCTTCGGAACAAGAGACCCCTGTGAGCAAGGCATTGCTTTGAAGTTATTAAGTCT 120
Oy 121 GTTGTCACAAAAAGACACTTATATGATGAGCAAGGTTCTTTTATCTTGCCAGATAT 180
Db 121 GTTGTCACAAAAAGACACTTATATGATGAGCAAGGTTCTTTTATCTTGCCAGATAT 180
Oy 181 ATTATGACTAAACGATTATATGATGAGCAACATATTTGTAATTTGTTCAATGAT 240
Db 181 ATTATGACTAAACGATTATATGATGAGCAACATATTTGTAATTTGTTCAATGAT 240
Oy 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGGAAGAGCACAAGAAATATAT 300
Db 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGGAAGAGCACAAGAAATATAT 300
Oy 301 ACCATGATCTACAGAACTTGTAGTATGATCAATCAGCAGAAATATCGACTCAGTACA 360
Db 301 ACCATGATCTACAGAACTTGTAGTATGATCAATCAGCAGAAATATCGACTCAGTACA 360
Oy 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGGTGGAGTAT 402
Db 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGGTGGAGTAT 402

RESULT 10
AX695559 1476 bp DNA linear PAT 31-MAR-2003
LOCUS AX695559
DEFINITION Sequence 1186 from Patent WO03008583.
ACCESSION AX695559
VERSION AX695559.1 GI:29418711
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Morris, D.W. and Engelhard, E.K.
AUTHORS Novel compositions and methods for cancer
TITLE Patent: WO 03008583-A 1186 30-JUN-2003;
JOURNAL Segre's Discovery (US)
FEATURES location/Qualifiers
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ORIGIN

/db_xref="taxon:9606"

Query Match 100.0%; Score 402; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2,3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGCTGTACCTAGTGTGCTGTACCTGACCTGACCTGACAGATTCCA 60
DB 1 ATGTGCAATACCAACATGCTGTACCTAGTGTGCTGTACCTGACCTGACCTGACAGATTCCA 60
QY 61 GCTTGGGAACAAGAGACCCGTGTAGACCAAGGCAATGCTTTTGAAGTATTAATATCT 120
DB 61 GCTTGGGAACAAGAGACCCGTGTAGACCAAGGCAATGCTTTTGAAGTATTAATATCT 120
QY 121 GTTGTGACACAAAAGACACTTATATCTATGAGAAAGATTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGTGACACAAAAGACACTTATATCTATGAGAAAGATTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGATATTTGTTCAATGAT 240
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QY 241 CTCTAGAGATTGTTGCGGTGCGCAAGCTTCTCTGTGAAAGCAAGGAAATATAT 300
DB 241 CTCTAGAGATTGTTGCGGTGCGCAAGCTTCTCTGTGAAAGCAAGGAAATATAT 300
QY 301 ACCATGATCTACAGAACTTGTGTAGTGTGATGATGATGATGATGATGATGATGATGAT 360
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QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGAGATGAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGAGATGAT 402

RESULT 11

BT007258

LOCUS

BT007258 1476 bp mRNA linear PRI 13-MAY-2003

Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53

BT007258.1 GI:30583354

FLI CDNA.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Kauline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Pheilan,M. and Farmer,A.

Cloning of human full-length CDS in BD Creator(TM) System Donor

vector

Unpublished

2 (bases 1 to 1476)

Kauline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Pheilan,M. and Farmer,A.

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow

Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length

expression clones generated by BD Biosciences Clontech and the

Harvard Institute of Proteomics. Each CDS has been cloned and the

forms: with and without stop-codon (to allow fusion with C-terminal

tag). The CDS has been directionally cloned using BD in-Fusion(TM)

cloning system between the SalI and HindIII sites of the pDNR-DUAL

vector. Additional sequences in the clone: 'ACC' after SalI site

and before 'ATG' to provide Kozak consensus sequence; 'GG' after

last codon and before HindIII site to maintain reading frame.

SOURCE

1. 1476

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GH00203X1.0"

/clone_1ib="BD Creator(TM) CDS library derived from MGC

collection"

/lab_host="DH5alpha T1 resistant"

/note="Vector: pDNR-Dual1"

1. 1476

/codon_start=1

/product="Mdm2, transformed 3T3 cell double minute 2, p53

binding protein (mouse)"

/protein_id="AAP35922.1"

/db_xref="GI:30583355"

/translation="MCTNMNSVPTDGAATTSQIPASEQETLVKPKPLKLSKVGAG

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RRRAISLETBNSDELSEGRQKHKSDISLSFDESLACVIREICERSSSSESTGT

PSNPDLDAVSEHSQMDLDQDSVSDQSVSEFESLSDSDYLSSEGOELSDDEIV

QVTVYQAGSDTDSFEDEPEISLADYWKCTSCNENPPLPSHCNRCMALREMLPEDK

GDKGELISEKAKLNSSTQAEFGDVPDCKITIVNDSRSCVENEDKXITQASQOSE

DYSOPSTSSIIYSSQEDYKEPERETDQKESVESLPLNMLEPVCIGGRKNCI

VHKTHLMACTCAKAKLKKRKPCCVCRPIOMIVLTTPP"

ORIGIN

Query Match 100.0%; Score 402; DB 9; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2,3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGCTGTACCTAGTGTGCTGTACCACTGACAGATTCCA 60
DB 1 ATGTGCAATACCAACATGCTGTACCTAGTGTGCTGTACCACTGACAGATTCCA 60
QY 61 GCTTGGGAACAAGAGACCCGTGTAGACCAAGGCAATGCTTTTGAAGTATTAATATCT 120
DB 61 GCTTGGGAACAAGAGACCCGTGTAGACCAAGGCAATGCTTTTGAAGTATTAATATCT 120
QY 121 GTTGTGACACAAAAGACACTTATATCTATGAGAAAGATTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGTGACACAAAAGACACTTATATCTATGAGAAAGATTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGATATTTGTTCAATGAT 240
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QY 241 CTCTAGAGATTGTTGCGGTGCGCAAGCTTCTCTGTGAAAGCAAGGAAATATAT 300
DB 241 CTCTAGAGATTGTTGCGGTGCGCAAGCTTCTCTGTGAAAGCAAGGAAATATAT 300
QY 301 ACCATGATCTACAGAACTTGTGTAGTGTGATGATGATGATGATGATGATGATGATGAT 360
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QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGAGATGAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGAGATGAT 402

RESULT 12

BT007935

LOCUS

BT007935 1476 bp mRNA linear SYN 13-MAY-2003

Synthetic construct Homo sapiens Mdm2, transformed 3T3 cell double

minute 2, p53 binding protein (mouse) mRNA, partial cde.

BT007935.1 GI:30584708

FLI CDNA.

Synthetic construct

artificial sequences.

1 (bases 1 to 1476)

Kauline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Pheilan,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Pheilan,M. and Farmer,A.

FEATURES

Location/Qualifiers

| TITLE | JOURNAL | REFERENCE | AUTHORS |
|--|-------------|---------------------|---|
| Cloning of human full-length CDSs in BD Creator (TM) System Donor vector | Unpublished | 2 (bases 1 to 1476) | Phelan, M. and Farmer, A. |
| | | | Kaundinya, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kunda, N., Raphael, J., Morel, D., Kelley, T., Labaer, J., Lin, Y., Phelan, M. and Farmer, A. |
| | | | Direct Submission |
| | | | Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA |
| | | | This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD in-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/otfclones . |

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FEATURES
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        location/Qualifiers
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RRRIISRETNDELSEGRORKRHKRSDISLSPESLALCYIRICCRSSSSSTGT
PSRNDLDAVSEHSGDWLDDQDSVSDGVSVEVESLSEDEYSLSSEGEGLSDEDEYV
QVTVYQAGESDTDSFEEDPEISLADYQKSCNEMNPLPEHCNRCAVLRNNWLPEDR
GKDGSEISERAKLENTSQOAEGFDPVDCIKTIVNDSRECYENNDKITQASQSESE
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VHGKTHGLMACFTCAKKLKRRNKCPCVCRDPTQMIIVLTYPPL"

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| Query Match | 100.0% | Score 402 | DB 12 | Length 1476 |
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| QY | 1 | ATGTGCATATCCACATGTCCTGTACTATGSGTGTACCACTCCACAGATTCCA | 60 | |
| Db | 1 | ATGTGCATATCCACATGTCCTGTACTATGSGTGTACCACTCCACAGATTCCA | 60 | |
| QY | 61 | GCTTCGGAACAAGAGACCCCTGGTTAGACCAAAAGCATTCTTTTGAAGTTATTTAAAGTCT | 120 | |
| Db | 61 | GCTTCGGAACAAGAGACCCCTGGTTAGACCAAAAGCATTCTTTTGAAGTTATTTAAAGTCT | 120 | |
| QY | 121 | GTTGGTGCAAAAAGACCTTATATCTATGAAAGGTTCTTTTATCTTGGCCAGTAT | 180 | |
| Db | 121 | GTTGGTGCAAAAAGACCTTATATCTATGAAAGGTTCTTTTATCTTGGCCAGTAT | 180 | |
| QY | 181 | ATTATGACTAAACGATTATATGATGAGAAGCAACAATATTGTATATTGTTCAAATGAT | 240 | |
| Db | 181 | ATTATGACTAAACGATTATATGATGAGAAGCAACAATATTGTATATTGTTCAAATGAT | 240 | |
| QY | 241 | CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGGAANAAGCACAGGAAATATAT | 300 | |
| Db | 241 | CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGGAANAAGCACAGGAAATATAT | 300 | |

| QY | 301 | ACCATGATCTTACAGAACTTGTTAGTGTCAATACAGAGAAATATGGATCTCAGGTACA | 360 |
|----|-----|--|-----|
| Dd | 301 | ACCATGATCTTACAGAACTTGTTAGTGTCAATACAGAGAAATATGGATCTCAGGTACA | 360 |
| QY | 361 | TCCTGTGATGGAACAGGGTGCACCTTGAAGTGGAGTGAT | 402 |
| Dd | 361 | TCCTGTGATGGAACAGGGTGCACCTTGAAGTGGAGTGAT | 402 |

| | |
|------------|--------------------------------------|
| RESULT | 13 |
| LOCUS | CQ17844 |
| DEFINITION | Sequence 3778 from Patent WO0206579. |
| ACCESSION | CQ17844 |
| VERSION | CQ17844.1 |
| KEYWORDS | GI:42278701 |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| PAT | 03-FEB-2004 |
| DNA | linear |

| REFERENCE | AUTHORS | TITLE | JOURNAL | FEATURES | SOURCE |
|-----------|---|--|----------------------------------|--|--------------------------|
| 1 | Venter, C. J., Adams, M. C., Li, P. W. and Myers, E. W. | kitas, such as nucleic acid arrays, comprising a majority of hexanucleotides or transcripts, for detecting expression and other uses thereof | WO 02068579-A, 3778 06-SEP-2002; | Patent: WO 02068579-A, 3778 06-SEP-2002; | PE Corporation (NY) (US) |
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| Best Local Similarity | 100.0%; | Pred. No. 2.2e-93; | | |
| Matches 402; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

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|----|-----|--------------|-------------|------------|--------------|-------------|-----|
| Qy | 1 | TTGGCAATACCA | CAGTCTGTAT | CCATACGATG | CTGTAAACACTG | CAATATCA | 60 |
| Db | 306 | ATGGCAATACCA | CAGTCTGTAT | CCATACGATG | CTGTAAACACTG | CAAGATTCA | 365 |
| Qy | 61 | GCTTGGCAACAG | AGACCCCTGGT | TAGACCAAGC | CAATGCTTTGA | AGTTAAAGTCT | 120 |
| Db | 366 | GCTTGGCAACAG | AGACCCCTGGT | TAGACCAAGC | CAATGCTTTGA | AGTTAAAGTCT | 425 |
| Qy | 121 | GTTCGGTCA | CAAAAAGAC | CACTTATAT | ATAGAAAGAG | GTTCCTTTTAA | 180 |
| | | | | | | | |

| | | | |
|----------------|-----|--|-----|
| D _b | 426 | GTGGTGCCACAAAAGACATTATACATGTGAAGAGGCTCTTTTATCTTGGCCAGAT | 485 |
| Q _Y | 181 | ATTATGACTAAACGATTATATATGATGAAGAACCAACACATATTTGATATTTGTTCCAAATCAT | 240 |
| D _b | 486 | ATTATGACTAAACGATTATATATGATGAAGAACCAACACATATTTGATATTTGTTCCAAATCAT | 545 |
| Q _Y | 241 | CTTCTAGAGATTTGTTTGGCGTGCCAAAGCTTCTCTGTGAAGAGGCAACAGAAATATAT | 300 |
| D _b | 546 | CTTCTAGAGATTTGTTTGGCGTGCCAAAGCTTCTCTGTGAAGAGGCAACAGAAATATAT | 605 |

Qy 301 ACCATGATCTACAGGAACCTTGAGTAGTCGAATCAGCAGGAATCATCGSACTCAGGTACA 360
|||
Db 606 ACCATGATCTACAGGAACCTTGAGTAGTCGAATCAGCAGGAATCATCGSACTCAGGTACA 665
Qy 361 TCTGTGATGAGGAACAGGTGCACTCTGAAGAGGTGGAGTAT 402
|||
Db 666 TCTGTGATGAGGAACAGGTGCACTCTGAAGAGGTGGAGTAT 707

| | | | | | |
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| RESULT 14 | | | | | |
| AR000256 | AR000256 | 2372 bp | DNA | linear | PAT 04-DEC-1998 |
| LOCUS | Sequence 2 from patent US 5736338. | | | | |
| DEFINITION | | | | | |
| ACCESSION | AR000256 | | | | |

VERSION AR000256.1 GI:3962787
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burdell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Method of diagnosing Neoplastic disease by detecting increased
expression of human MDM2 protein
JOURNAL Patent: US 576338-A 2 07-Apr-1998;
FEATURES Location/Qualifiers
Source 1..2372
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/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 2.2e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGTGTGTAAACCACTTCACGATTCCA 60
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QY 61 GCTTCGGAACAAAGACCTGTGTGAACAAAGCCATTGCTTTGAAGTTATTAAAGTCT 120
DB 372 GCTTCGGAACAAAGACCTGTGTGAACAAAGCCATTGCTTTGAAGTTATTAAAGTCT 431
QY 121 GTTGTGACAAAAAAGACATTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACAAAAAAGACATTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 240
DB 492 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTAGTATCAATCAGAGAAATCATCGACTCAGGTACA 360
DB 612 ACCATGATCTACAGAACTTGTAGTATCAATCAGAGAAATCATCGACTCAGGTACA 671
QY 361 TCTGTAGTGAGAAACAGGTGTCACTTGAAGGTGGAGTGAT 402
DB 672 TCTGTAGTGAGAAACAGGTGTCACTTGAAGGTGGAGTGAT 713

RESULT 15

AR009781 AR009781 2372 bp DNA linear PAT 04-DEC-1998
LOCUS AR009781
DEFINITION Sequence 2 from patent US 5756455.
ACCESSION AR009781
VERSION AR009781.1 GI:3968586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5756455-A 2 26-MAY-1998;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 2.2e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGTGTGTAAACCACTTCACGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACTACTGATGTGTGTAAACCACTTCACGATTCCA 371
QY 61 GCTTCGGAACAAAGACCTGTGTGAACAAAGCCATTGCTTTGAAGTTATTAAAGTCT 120
DB 372 GCTTCGGAACAAAGACCTGTGTGAACAAAGCCATTGCTTTGAAGTTATTAAAGTCT 431
QY 121 GTTGTGACAAAAAAGACATTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACAAAAAAGACATTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 240
DB 492 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
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DB 612 ACCATGATCTACAGAACTTGTAGTATCAATCAGAGAAATCATCGACTCAGGTACA 671
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DB 672 TCTGTAGTGAGAAACAGGTGTCACTTGAAGGTGGAGTGAT 713

Search completed: October 18, 2004, 12:49:33
Job time : 2820 secs

PS Disclosure; Fig 2A; 78pp; English.

XX
CC The present sequence encodes a fragment of a human MDM2 polypeptide,
CC which binds to a human MDM2 interacting polypeptide (MDMIP). The protein
CC fragment was used as bait in a yeast two hybrid system to identify MDMIP.
CC The MDMIP polypeptide is useful for detecting and removing MDM2
CC polypeptides in a biological sample by forming MDM2-MDMIP complexes.
CC MDMIP and MDM2 are useful to identify compounds or other agents which
CC modulate the activity of MDM2 and/or MDMIP-mediated processes. Agents
CC that modulate the function of MDMIP/MDM2 complexes are useful for
CC treating and preventing a disease or disorder involving aberrant levels
CC of MDM2 or MDMIP. MDMIP is also useful for treating diseases caused by
CC aberrant levels of expression of MDM2 genes, such as disorders of cell
CC cycle progression, cell differentiation, and transcriptional control,
CC including cancers such as human sarcoma, glioma, squamous cell carcinoma,
CC breast cancer, astrocytoma, leukemia and lymphoma, and tumorigenesis.
CC MDMIP and MDM2 nucleic acids are useful in gene therapy

XX
SQ Sequence 652 BP; 212 A; 116 C; 145 G; 179 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 3; Length 652;

Best Local Similarity 100.0%; Pred. No. 1.9e-106; Mismatches 0; Gaps 0;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTTACTGATGCTGTAAACACCTCAGATTCCA 60
Db 1 ATGTGCAATACCAACATGTCTGTACCTTACTGATGCTGTAAACACCTCAGATTCCA 60

QY 61 GCTTCGGAACAAAGAGACCTGTGTTAGCCAAAGCCATTGCTTTGAAGTTATTAACTCT 120
Db 61 GCTTCGGAACAAAGAGACCTGTGTTAGCCAAAGCCATTGCTTTGAAGTTATTAACTCT 120

QY 121 GTTGTGTCACAAAAGACACTTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 180
Db 121 GTTGTGTCACAAAAGACACTTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 180

QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 240
Db 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 240

QY 241 CTTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGCAAGCAAAATATAT 300
Db 241 CTTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGCAAGCAAAATATAT 300

QY 301 ACCATGATCTACAGAACTTGTAGTCAATCAGAGCAATATGAGCTCAGGTACA 360
Db 301 ACCATGATCTACAGAACTTGTAGTCAATCAGAGCAATATGAGCTCAGGTACA 360

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

RESULT 2
ID AA092515 standard; DNA; 852 BP.

XX AA092515;

XX 02-FEB-1996 (first entry)

XX Human double minute gene 2 (hdm-2) fragment 1.

XX Human double minute gene 2; hdm-2; antibody binding region; antigen;

XX cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunosassay; ss.

XX Homo sapiens.

XX Key location/Qualifiers

XX CDS 1..852
FT /"tag= a
FT /label= Fragment_1
FT /note= "encodes amino acids 1-284 of hdm-2, i.e. the 5'-

FT region of the ORF only"

XX DE4339533-A1.

XX 14-JUN-1995.

XX 19-NOV-1993; 93DE-04339533.

XX 19-NOV-1993; 93DE-04339533.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Zentgraf H, Klein R, Frey M, Martens R;

XX WPL; 1995-216248/29.

XX P-PSDB; AAR75494.

XX Detection of human double minute gene 2 (hdm-2) antibodies - by

XX the detection of specific cancers.

XX Claim 13; Fig 2; 12pp; German.

XX DNA fragments coding for amino acids 1-284, 58-284 and 58-491 of the hdm-

XX 2 (human double minute 2) gene product are claimed. The overlapping

XX protein fragments contain binding regions for hdm-2-specific antibodies

XX and are useful for identifying such antibodies using a claimed

XX immunosassay method. The presence of anti-hdm-2 antibodies is diagnostic

XX of certain forms of cancer, e.g. rhabdomyosarcoma

XX Sequence 852 BP; 271 A; 145 C; 199 G; 237 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 852;

Best Local Similarity 100.0%; Pred. No. 2e-106;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTTACTGATGCTGTAAACACCTCAGATTCCA 60
Db 1 ATGTGCAATACCAACATGTCTGTACCTTACTGATGCTGTAAACACCTCAGATTCCA 60

QY 61 GCTTCGGAACAAAGAGACCTGTGTTAGCCAAAGCCATTGCTTTGAAGTTATTAACTCT 120
Db 61 GCTTCGGAACAAAGAGACCTGTGTTAGCCAAAGCCATTGCTTTGAAGTTATTAACTCT 120

QY 121 GTTGTGTCACAAAAGACACTTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 180
Db 121 GTTGTGTCACAAAAGACACTTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 180

QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 240
Db 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTGTTCAATGAT 240

QY 241 CTTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGCAAGCAAAATATAT 300
Db 241 CTTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGCAAGCAAAATATAT 300

QY 301 ACCATGATCTACAGAACTTGTAGTCAATCAGAGCAATATGAGCTCAGGTACA 360
Db 301 ACCATGATCTACAGAACTTGTAGTCAATCAGAGCAATATGAGCTCAGGTACA 360

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

RESULT 3
ID AA087261 standard; DNA; 852 BP.

XX AA087261;

XX 25-MAR-2003 (revised)

XX 25-JUN-1996 (first entry)

XX Key location/Qualifiers

XX CDS 1..852
FT /"tag= a
FT /label= Fragment_1
FT /note= "encodes amino acids 1-284 of hdm-2, i.e. the 5'-

```

XX DE Human double minute gene 2 (hdm-2) fragment 1.
XX KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
XX KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; ss.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT 1..852
XX FT CDS /*tag= a
FT /label= Fragment_1
FT /note= "encodes amino acids 1-284 of hdm-2, i.e. the 5'-
FT region of the ORF only"
XX DE DE345249-A1.
XX PN 24-MAY-1995.
XX PD 19-NOV-1993; 93DE-04345249.
XX PF 19-NOV-1993; 93DE-04345249.
XX PR 19-NOV-1993; 93DE-04339533.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PI Zentgraf H, Klein R, Frey M, Martens R;
XX DR WPI; 1995-195167/26.
XX DR P-PSDB; AAR75397.
XX PT New hdm-2 fragments contg. antibody binding region - used to detect
XX PT specific antibodies for diagnosis of cancers, also new DNA sequences
XX PT encoding them.
XX PS Claim 4; Fig 2; 11pp; German.
XX CC DNA fragments coding for amino acids 1-284, 58-284 and 58-491 of the hdm-
XX CC 2 (human double minute 2) gene product are claimed. The overlapping
XX CC protein fragments contain binding regions for hdm-2-specific antibodies
XX CC and are useful for identifying such antibodies. The presence of anti-hdm-
XX CC 2 antibodies is diagnostic of certain forms of cancer, e.g.
XX CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX SO Sequence 852 BP; 271 A; 145 C; 199 G; 237 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAATACCAATGTCGTCTGTAACCTGCTGTAACCACTTCACAGATTCCA 60
DB 1 ATGTCGAATACCAATGTCGTCTGTAACCTGCTGTAACCACTTCACAGATTCCA 60
QY 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAAAGCATTGCTTTGAAGTTATTAAGTCT 120
DB 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAAAGCATTGCTTTGAAGTTATTAAGTCT 120
QY 121 GTTGTGCACAAAAGACACTTATATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGTGCACAAAAGACACTTATATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACATATATATGATGAGAAAGCAACATATTTGTTCAAAAGAT 240
DB 181 ATTATGACTAAACATATATATGATGAGAAAGCAACATATTTGTTCAAAAGAT 240
QY 241 CTTTGTAGAGATTGTTGGTGGTCCAAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
DB 241 CTTTGTAGAGATTGTTGGTGGTCCAAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
QY 301 ACCATGATCTACAGAAAGCTTGTAGTATGTCATACAGAGAAATATCGGACTCAGTACA 360
DB 301 ACCATGATCTACAGAAAGCTTGTAGTATGTCATACAGAGAAATATCGGACTCAGTACA 360

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QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTAT 402

RESULT 4
ID AAT61637 standard; cDNA; 1476 BP.
XX AAT61637
XX AC AAT61637;
XX DT 16-JAN-1998 (first entry)
XX DE Murine double minute 2 coding sequence.
XX KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX KW restenosis; ss.
XX OS Mus musculus.
XX PN WO9709343-A2.
XX PD 13-MAR-1997.
XX PF 02-SEP-1996; 96WO-FR001340.
XX PR 04-SEP-1995; 95FR-00010331.
XX PA (RHON) RHONE-POULENC RORER SA.
XX PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX PI Tocque B, Duba-Poterezman M, Wasylyk B;
XX DR WPI; 1997-192837/17.
XX DR P-PSDB; AAM13600.
XX PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
XX PT or nucleic acid encoding an antagonist, also viral vectors contg. this
XX PT nucleic acid.
XX PS Claim 2; Page 26-30; 43pp; French.
XX CC This is the nucleotide sequence encoding the mouse Mdm2 (murine double
XX CC minute-2) protein, a 90 kD phosphoprotein which binds and modulates the
XX CC activity of the tumour suppressor protein p53. It has now been shown that
XX CC the mdm2 protein itself has oncogenic properties, especially in a p53-
XX CC null background. Mdm2 is observed to unblock cell cycle arrest in G1
XX CC caused by over-expression of the p107 protein. This is especially done by
XX CC the region covering amino acid 1-134. The invention therefore relates to
XX CC antagonists able to inhibit the oncogenic activity of mdm2. These include
XX CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
XX CC -25 or 18-23 (AAM13602-6), or fragments of transcription factors e.g.
XX CC TBP, TBP or TBP250, which bind amino acids 1-134 of mdm2. Other
XX CC inhibitors include compounds which disrupt binding to region 135-491 of
XX CC mdm2, e.g. Rb, U5 or the transcription factor E2F. The antagonists are
XX CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
XX CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other
XX CC hyperproliferative conditions such as restenosis
XX SO Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAATACCAATGTCGTCTGTAACCTGCTGTAACCACTTCACAGATTCCA 60
DB 1 ATGTCGAATACCAATGTCGTCTGTAACCTGCTGTAACCACTTCACAGATTCCA 60
QY 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAAAGCATTGCTTTGAAGTTATTAAGTCT 120

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Db      61 GCTTCGGAACAGAGACCCGTGTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
Qy      121 GTTGTGCACAAAAGACACTTATACATATGAAAAGGTCCTTTTATCTTGGCAGTAT 180
Db      121 GTTGTGCACAAAAGACACTTATACATATGAAAAGGTCCTTTTATCTTGGCAGTAT 180
Qy      181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTATTTGTCAAATGAT 240
Db      181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTATTTGTCAAATGAT 240
Qy      241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGCAACAGAAAATATAT 300
Db      241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGCAACAGAAAATATAT 300
Qy      301 ACCATGATCTACAGGAACCTGTAGTATGATCATGACAGAGATATCGAAGTCACTCA 360
Db      301 ACCATGATCTACAGGAACCTGTAGTATGATCATGACAGAGATATCGAAGTCACTCA 360
Qy      361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
Db      361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
```

RESULT 5
AAC84596
ID AAC84596 standard; DNA; 1476 BP.

AC AAC84596;
XX
DT 02-APR-2001 (first entry)
XX

DE Human MDM2 protein encoding DNA.

KM S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytosolic; ds.

XX Homo sapiens.

XX NO200075184-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000MO-US015449.

XX 04-JUN-1999; 99US-0137494P.

XX (UYVA) UNIV YALE.

PI Zhang H, Tsvetkov LM, Kondo T;

DR WPI; 2001-061703/07.

DR P-PSDB; AAB48284.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins.

XX Example; Page 93-95; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
XX cell, using proteins selected from S-phase kinase associated proteins 1
XX and 2 (SKP1, SKP2), SKP2-like proteins (ZP) and CUL-1 (a member of the
XX cullin/CDC53 family of proteins). The method is useful for altering the
XX level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
XX detecting tumours, and in monitoring tumor treatment in a mammal. Agents
XX that modulate interactions between SKP and target proteins are useful for
XX treating tumours

XX Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 4; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGTGCATTCACCAACATGCTGTGACTACTGATGCTGTGTAACCACTTCACGATTTCCA 60
Db      1 ATGTGCATTCACCAACATGCTGTGACTACTGATGCTGTGTAACCACTTCACGATTTCCA 60
Qy      61 GCTTCGGAACAGAGACCCGTGTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
Db      61 GCTTCGGAACAGAGACCCGTGTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
Qy      121 GTTGTGCACAAAAGACACTTATACATATGAAAAGGTCCTTTTATCTTGGCAGTAT 180
Db      121 GTTGTGCACAAAAGACACTTATACATATGAAAAGGTCCTTTTATCTTGGCAGTAT 180
Qy      181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTATTTGTCAAATGAT 240
Db      181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTATTTGTCAAATGAT 240
Qy      241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGCAACAGAAAATATAT 300
Db      241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGCAACAGAAAATATAT 300
Qy      301 ACCATGATCTACAGGAACCTGTAGTATGATCATGACAGAGATATCGAAGTCACTCA 360
Db      301 ACCATGATCTACAGGAACCTGTAGTATGATCATGACAGAGATATCGAAGTCACTCA 360
Qy      361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
Db      361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
```

RESULT 6
ADA02668
ID ADA02668 standard; cDNA; 1476 BP.

AC ADA02668;

XX 06-NOV-2003 (first entry)

DE Human MDM2 carcinoma associated coding sequence, SEQ ID NO:1186.

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;

XX prostate; lymphoma; leukemia; cytosolic; gene therapy; drug screening;

XX gene; ss.

XX Homo sapiens.

XX NO2003057146-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002MO-US041414.

XX 26-DEC-2001; 2001US-00035832.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-587068/55.

XX New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.

XX Claim 1; SEQ ID NO 1186; 245pp; English.

XX The invention relates to recombinant carcinoma associated (CA) nucleic
XX acid sequences from mouse and human (ADA01482-ADA03094), and to
XX recombinant carcinoma associated proteins (CAP) encoded by them. The
XX invention also encompasses expression vectors and host cells comprising a
XX CA nucleic acid, a polypeptide (especially an antibody) that specifically

binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 9; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106; Mismatches 0; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGGCTGAACCACTCAGATTCCA 60
Db 1 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGGCTGAACCACTCAGATTCCA 60
Qy 61 GCTTCGGAACAAGAGACCCTGGTTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120
Db 61 GCTTCGGAACAAGAGACCCTGGTTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120
Qy 121 GTTGTGACACAAAGACACTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
Db 121 GTTGTGACACAAAGACACTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
Qy 181 ATTATGACTTAACGATTATATGATGAGAGCAACAAATATGTAATGTTCAATATAT 240
Db 181 ATTATGACTTAACGATTATATGATGAGAGCAACAAATATGTAATGTTCAATATAT 240
Qy 241 CTTTGAAGAGATTGTTTGGGTCGCAAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
Db 241 CTTTGAAGAGATTGTTTGGGTCGCAAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
Qy 301 ACCATGATCTACAGGAATTGGTAGTATGATCAATCAGCAGAAATCATCGAGTACA 360
Db 301 ACCATGATCTACAGGAATTGGTAGTATGATCAATCAGCAGAAATCATCGAGTACA 360
Qy 361 TCTGTGAGTGAGAACAGGTGTCACTTGAGAGTGGAGTAT 402
Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAGAGTGGAGTAT 402
```

RESULT 7
ID ADB72406 standard; cDNA; 1476 BP.

ADB72406;

04-DEC-2003 (first entry)

Human MDM2 cDNA.

human; ss; cytosolic; gene therapy; vaccine; carcinoma; lymphomas;
cancer; neoplasm; adenocarcinoma; sarcoma; gene.

Homo sapiens.

WO2003008583-A2.

30-JAN-2003.

26-DEC-2001; 2001WO-US051291.

02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00977722.
20-DEC-2001; 2001US-00034650.

(SAGR-) SAGRES DISCOVERY.

Morris DW, Engelhard EK;

WPI; 2003-239337/23.

New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
cancers, neoplasm, adenocarcinoma, or sarcomas.

Claim 1; SEQ ID NO 234; 2304bp; English.

The invention relates to a novel recombinant nucleic acid comprising a
nucleotide sequence selected from any of the 660 sequences fully defined
in the specification. A polynucleotide of the invention has cytosolic
activity, and may have a use in gene therapy, or in a vaccine. The
recombinant nucleic acids and polypeptides are useful for treating
carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
sarcomas. The present sequence represents a human cDNA of the invention.

Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 10; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106; Mismatches 0; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGGCTGAACCACTCAGATTCCA 60
Db 1 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGGCTGAACCACTCAGATTCCA 60
Qy 61 GCTTCGGAACAAGAGACCCTGGTTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120
Db 61 GCTTCGGAACAAGAGACCCTGGTTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120
Qy 121 GTTGTGACACAAAGACACTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
Db 121 GTTGTGACACAAAGACACTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
Qy 181 ATTATGACTTAACGATTATATGATGAGAGCAACAAATATGTAATGTTCAATATAT 240
Db 181 ATTATGACTTAACGATTATATGATGAGAGCAACAAATATGTAATGTTCAATATAT 240
Qy 241 CTTTGAAGAGATTGTTTGGGTCGCAAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
Db 241 CTTTGAAGAGATTGTTTGGGTCGCAAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
Qy 301 ACCATGATCTACAGGAATTGGTAGTATGATCAATCAGCAGAAATCATCGAGTACA 360
Db 301 ACCATGATCTACAGGAATTGGTAGTATGATCAATCAGCAGAAATCATCGAGTACA 360
Qy 361 TCTGTGAGTGAGAACAGGTGTCACTTGAGAGTGGAGTAT 402
Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAGAGTGGAGTAT 402
```

RESULT 8
ID ADB95916 standard; DNA; 1476 BP.

ADB95916;

12-FEB-2004 (first entry)

Human MDM2 gene coding sequence.

cancer diagnosis; cancer treatment; carcinoma; cytosolic; gene therapy;
lymphoma; breast cancer; prostate cancer; leukemia; ds; human; MDM2.

| | | |
|--|---|---|
| XX | OS | Homo sapiens. |
| XX | PN | WO2003039484-A2. |
| XX | PD | 15-MAY-2003. |
| XX | PF | 08-NOV-2002; 2002MO-US036071. |
| XX | PR | 08-NOV-2001; 2001US-00052482. |
| XX | PA | (SAGR-) SAGRES DISCOVERY. |
| XX | PI | Morris DW, Engelhard EK; |
| XX | DR | WPI; 2003-441462/41. |
| XX | PT | New carcinoma associated nucleic acids and proteins, useful for screening |
| XX | PT | drug candidates, or for diagnosing and treating carcinomas, e.g. |
| XX | PT | lymphoma, breast cancer, prostate cancer or leukemia. |
| XX | PS | Claim 1; SEQ ID NO 174; 793bp; English. |
| CC | CC | This invention relates to novel recombinant nucleic acids for use in |
| CC | CC | diagnosis and treatment of cancer, especially carcinomas, as well as the |
| CC | CC | use of compositions in screening methods. The compositions of the |
| CC | CC | invention may have cytotoxic activity whilst the disclosed sequences may |
| CC | CC | be useful for gene therapy. The carcinoma associated nucleic acids and |
| CC | CC | proteins are useful for diagnosing and treating carcinomas, for example |
| CC | CC | lymphoma, breast cancer, prostate cancer or leukaemia, or for screening |
| CC | CC | drug candidates or bioactive agents capable of binding to, or modulating |
| CC | CC | the activity of, a carcinoma associated protein. The present sequence is |
| CC | CC | the coding DNA sequence of the human MDM2 gene which is a carcinoma |
| CC | CC | associated gene of the invention. |
| SQ | SQ | Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other; |
| Query Match | 100.0%; Score 402; DB 10; Length 1476; | |
| Best Local Similarity | 100.0%; Pred. No. 2,56-106; | |
| Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| Oy | 1 ATGTGCATATACCAATGCTGTGTACTTCTGATGGTGCGTAAACACCATCAGATTCCA | 60 |
| Dd | 1 ATGTGCATATACCAATGCTGTGTACTTCTGATGGTGCGTAAACACCATCAGATTCCA | 60 |
| Oy | 61 GCTTCGAACAAGAGACCCTGGTTAGACCACCAAGCCATTGCTTTTAAGTTATAAAGTCT | 120 |
| Dd | 61 GCTTCGAACAAGAGACCCTGGTTAGACCACCAAGCCATTGCTTTTAAGTTATAAAGTCT | 120 |
| Oy | 121 GTTGGTGACAAAAGAAGACCTTATCTATGTAAGAGGTTCTTTTATCTTGGCCAGAT | 180 |
| Dd | 121 GTTGGTGACAAAAGAAGACCTTATCTATGTAAGAGGTTCTTTTATCTTGGCCAGAT | 180 |
| Oy | 181 ATTATGACTTAAACGATTATATGATAGAGAAGCAACAACATATTTGTTCAATGAT | 240 |
| Dd | 181 ATTATGACTTAAACGATTATATGATAGAGAAGCAACAACATATTTGTTCAATGAT | 240 |
| Oy | 241 CTTCAGAGATTGTTGGGCTGCCAAGCTTCTCTGTGAAGAGCACAGAAAAATATAT | 300 |
| Dd | 241 CTTCAGAGATTGTTGGGCTGCCAAGCTTCTCTGTGAAGAGCACAGAAAAATATAT | 300 |
| Oy | 301 ACCATGATCTACAGAACCTTGGTAGTAGTCAATAGCAGAGAAATCATCGGACTCAGGTACA | 360 |
| Dd | 301 ACCATGATCTACAGAACCTTGGTAGTAGTCAATAGCAGAGAAATCATCGGACTCAGGTACA | 360 |
| Oy | 361 TCTGTAGTAGAAGACAGGTGTCACTTGAAGGTGGAGATGAT 402 | |
| Dd | 361 TCTGTAGTAGAAGACAGGTGTCACTTGAAGGTGGAGATGAT 402 | |
| RESULT 9 | | |
| ID | ADN71935 | standard; cDNA; 2371 BP. |

| | | |
|---------------------------|---|---------------------|
| XX | AC | ADN71935; |
| XX | XX | |
| DT | 12-AUG-2004 | (first entry) |
| DE | MDM2 encoding cDNA SEQ ID NO:21. | |
| XX | XX | |
| KW | kinase pathway inhibitor; anti-prostate cancer; | |
| KW | mitogen-activated protein kinase pathway inhibitor; | |
| KW | MAP kinase pathway inhibitor; prostate cancer inhibitor; | |
| KW | phosphatidylinositol 3-kinase/Akt kinase pathway; | |
| KW | phosphatidylinositol 3-kinase pathway; cytosolic; MAP kinase inhibitor; | |
| KW | PI3K/Akt kinase inhibitor; 3-kinase/Akt kinase inhibitor; | |
| KW | PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer; | |
| XX | MDM2; gene; ss. | |
| OS | Unidentified. | |
| XX | XX | |
| FH | Key | Location/Qualifiers |
| FT | CDS | 311..1786 |
| FT | | /tag= a |
| FT | | /product= "MDM2" |
| PN | MO200404185-A2. | |
| XX | XX | |
| PD | 21-MAY-2004. | |
| PF | 31-OCT-2003; 2003WO-US034636. | |
| PR | 31-OCT-2002; 2002US-0423340P. | |
| PA | (UYRP) UNIV ROCHESTER. | |
| PI | Chang C, Lee Y, Lin W; | |
| PT | WP1: 2004-390508/36. | |
| DR | P-PSDB; ADN71936. | |
| XX | XX | |
| XX | Composition useful in the treatment of e.g. prostate cancer comprises a | |
| XX | kinase pathway inhibitor and an anti-prostate cancer compound. | |
| PS | Disclosure; SEQ ID NO 21; 118pp; English. | |
| XX | XX | |
| CC | The present invention describes a composition (C1) which comprises a | |
| CC | kinase pathway inhibitor (a) and an anti-prostate cancer compound (b). | |
| CC | Also described: (1) identification of a mitogen-activated protein (MAP) | |
| CC | kinase pathway inhibitor involving incubating an antiandrogen or a | |
| CC | library of molecules with a cell containing an activable MAP kinase | |
| CC | pathway and selecting the molecules which inhibit the activation of the | |
| CC | MAP kinase pathway; and (2) identification of a prostate cancer inhibitor | |
| CC | involving incubating a cell with hydroxyflutamide and potential | |
| CC | inhibitor, and assaying the level of activation of MAP kinase pathway or | |
| CC | phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has | |
| CC | cyclostatic activity, and can be used as a MAP kinase inhibitor, | |
| CC | phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen | |
| CC | receptor (AR) inhibitor. C1 can be used in the treatment of prostate | |
| CC | cancer; for identifying a MAP kinase pathway inhibitor; for identifying a | |
| CC | prostate cancer inhibitor; and for reducing the number of prostate cancer | |
| CC | cells in a sample. The composition C1 provides effective combination | |
| CC | therapy as compared to prior therapies. The present sequence encodes | |
| CC | MDM2, which is used in the exemplification of the present invention. | |
| XX | XX | |
| SQ | Sequence 2371 BP; 698 A; 490 C; 541 G; 642 T; 0 U; 0 Other; | |
| Query Match | 100.0%; Score 402; DB 12; Length 2371; | |
| Best Local Similarity | 100.0%; Pstd. No. 3e-106; | |
| Matches 402; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | |
| OY | 1 ATGTGGCAATTCGAATGTCGTACTGCACAGTATGTTGTAACCACTTCCA | 60 |
| db | | |
| | 311 ATGTGGCAATTCGAATGTCGTACTGCACAGTATGTTGTAACCACTTCCA | 370 |
| OY | 61 GCTTCGAAACAAGACCCTCGTGATGACCAAAGCATTCGTTTGAAGTTAAGTCT | 120 |

XX WPI; 1995-206312/27.
DR P-PSDB; AAR76696.
XX
XX New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT treatment of tumours.
XX
XX Claim 1; Col 19-24; 34pp; English.
XX
CC The human MDM2 gene is genetically altered (i.e. amplified) in human
CC tumour cells. Detecting that the gene has become amplified or detecting
CC increased gene product expression (using probes, proteins, antibodies and
CC inhibitors) allows diagnosis and therapy of cancers such as colorectal
CC carcinoma, lung cancer and chronic myelogenous leukaemia. The human MDM2
CC protein binds to human p53 and allows the cell to escape from p53-
CC regulated growth. (Updated on 16-Oct-2003 to standardise OS field)
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGTGCAATACCAACATGCTGTGACCTAGTGTGCTGTACACCTCAGATTCCA 60
DB 312 ATGTGCAATACCAACATGCTGTGACCTAGTGTGCTGTACACCTCAGATTCCA 371
QY 61 GCTTCGGAACAGAGACCTGCTGAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
DB 372 GCTTCGGAACAGAGACCTGCTGAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 431
QY 121 GTTGTGACACAAAAGACACTTATATGAGAAAGGCTTTTATCTTGGCAGTAT 180
DB 432 GTTGTGACACAAAAGACACTTATATGAGAAAGGCTTTTATCTTGGCAGTAT 491
QY 181 ATTATGACTTAACGATTATATGATGAGAGACAAACATATTTGTTCAATGAT 240
DB 492 ATTATGACTTAACGATTATATGATGAGAGACAAACATATTTGTTCAATGAT 551
QY 241 CTCTAGAGATTGTTGGGCGCCAAAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
DB 552 CTCTAGAGATTGTTGGGCGCCAAAGCTTCTCTGTAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCATCAGCAGAGATCATCGACTCAGTACA 360
DB 612 ACCATGATCTACAGAACTTGTAGTAGTCATCAGCAGAGATCATCGACTCAGTACA 671
QY 361 TCTGTGAGTGAGAAACAGGTGTACCTTGAAAGTGGAGTAT 402
DB 672 TCTGTGAGTGAGAAACAGGTGTACCTTGAAAGTGGAGTAT 713
XX
RESULT 12
AAT45151
ID AAT45151 standard; cDNA; 2372 BP.
XX
XX AAT45151;
XX
DT 25-MAR-2003 (revised)
DT 28-JUN-1997 (first entry)
XX
DE Human MDM-2 gene cDNA clone, involved in tumour-development.
XX
XX p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
XX antibody fusion protein; therapy; dr.
XX
XX Homo sapiens.
XX
XX OS
XX Key Location/Qualifiers
FH 312..1787
FT CDS /*tag= a
XX
XX US5550023-A.
XX
PN

XX
PD 27-AUG-1996.
XX
XX 18-MAY-1994; 94US-00245500.
PF
XX 07-APR-1992; 92US-00867840.
XX
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW;
XX
XX WPI; 1996-401591/40.
DR P-PSDB; AAW07887.
XX
XX
PT Identification of cpds. interfering with human MDM2/p53 binding - useful
PT as therapeutic agents to treat human neoplastic cells.
XX
XX
XX Example 1; Col 21-26; 36pp; English.
XX
CC AAT45151 is a cDNA clone of the human MDM-2 gene derived from a human
CC colon carcinoma cell line Caco-2. The MDM-2 protein produced by this
CC clone is used in a method for identifying compounds that interfere with
CC the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2
CC protein releases a cell from p53-regulated growth, allowing cancers to
CC develop. Therefore compounds identified as interfering with the binding
CC of MDM-2 to p53 are potentially useful in the treatment of human
CC neoplastic cells. In the method pref. one or both of the proteins is a
CC fusion protein esp. with an antibody or antibody fragment which aids
CC separation and identification. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGTGCAATACCAACATGCTGTGACCTAGTGTGCTGTACACCTCAGATTCCA 60
DB 312 ATGTGCAATACCAACATGCTGTGACCTAGTGTGCTGTACACCTCAGATTCCA 371
QY 61 GCTTCGGAACAGAGACCTGCTGAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
DB 372 GCTTCGGAACAGAGACCTGCTGAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 431
QY 121 GTTGTGACACAAAAGACACTTATATGAGAAAGGCTTTTATCTTGGCAGTAT 180
DB 432 GTTGTGACACAAAAGACACTTATATGAGAAAGGCTTTTATCTTGGCAGTAT 491
QY 181 ATTATGACTTAACGATTATATGATGAGAGACAAACATATTTGTTCAATGAT 240
DB 492 ATTATGACTTAACGATTATATGATGAGAGACAAACATATTTGTTCAATGAT 551
QY 241 CTCTAGAGATTGTTGGGCGCCAAAGCTTCTCTGTAAGAGCAGAGAAATATAT 300
DB 552 CTCTAGAGATTGTTGGGCGCCAAAGCTTCTCTGTAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCATCAGCAGAGATCATCGACTCAGTACA 360
DB 612 ACCATGATCTACAGAACTTGTAGTAGTCATCAGCAGAGATCATCGACTCAGTACA 671
QY 361 TCTGTGAGTGAGAAACAGGTGTACCTTGAAAGTGGAGTAT 402
DB 672 TCTGTGAGTGAGAAACAGGTGTACCTTGAAAGTGGAGTAT 713
XX
RESULT 13
AAT66410
ID AAT66410 standard; cDNA; 2372 BP.
XX
XX AAT66410;
XX
AC

```
XX 25-MAR-2003 (revised)
DT 14-SEP-2000 (revised)
DT 18-JUN-1997 (first entry)
XX
DE Human MDM2 coding sequence.
XX
KM Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KM p53-regulated growth; db.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 312..1787
XX FT CDS /*tag= a
XX FT /product= "MDM2"
XX
XX US5618921-A.
XX
XX PD 08-APR-1997.
XX
XX PF 17-FEB-1995; 95US-00390479.
XX
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelestein B, Kinzler KW, Burrell M, Hill DE;
XX WPI: 1997-225474/20.
XX DR P-PSDB; AAM15463.
XX
XX PT Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX PS Claim 1; Col 19-24; 35pp; English.
XX
XX CC This sequence encodes the human MDM2 protein. Antibodies that
XX specifically bind to human MDM2 protein may be used for detecting
XX elevated expression of the MDM2 gene in a human tissue or body fluid
XX sample, esp. for cancer diagnosis. The antibodies may be used to
XX interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
XX to sequester p53 and allow the cell to escape from p53-regulated growth.
XX (N.B. Revised record issued to correct the sequence analysis field.)
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SO Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACCACTCACAAGATTCCA 60
DB |||||||
DB 312 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACCACTCACAAGATTCCA 371
OY 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB |||||||
DB 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
OY 121 GTTGTGTGACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCCAGTAT 180
DB |||||||
DB 432 GTTGTGTGACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCCAGTAT 491
OY 181 ATTAATGACTTAACGATTTATATGATGAGAAGCAACAATATTGTATTGTTCAAAATGAT 240
DB |||||||
DB 492 ATTAATGACTTAACGATTTATATGATGAGAAGCAACAACAATATTGTATTGTTCAAAATGAT 551
OY 241 CTTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAAGACACAGGAAATATAT 300
DB |||||||
DB 552 CTTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAAGACACAGGAAATATAT 611
```

```
OY 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGGAATCATCGACTCAGGTACA 360
DB |||||||
DB 612 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGGAATCATCGACTCAGGTACA 671
OY 361 TCTGTGAGTGAGAAACAGGTGTACCTTGAAAGTGGAGTGTAT 402
DB |||||||
DB 672 TCTGTGAGTGAGAAACAGGTGTACCTTGAAAGTGGAGTGTAT 713

RESULT 14
AAT62065
ID AAT62065 standard; cDNA; 2372 BP.
XX
XX AC AAT62065;
XX
XX DT 25-MAR-2003 (revised)
XX DT 05-JUN-1997 (first entry)
XX
XX DE Human MDM2 cDNA.
XX
XX KM Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
XX elevation; expression; diagnosis; neoplasia; neoplastic transformation;
XX sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia; db.
XX
XX OS Homo sapiens.
XX
XX FT Key Location/Qualifiers
XX FT 312..1787
XX FT CDS /*tag= a
XX FT /product= "MDM2"
XX
XX PN US5606044-A.
XX
XX PD 25-FEB-1997.
XX
XX PF 17-FEB-1995; 95US-00390546.
XX
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Kinzler KW, Vogelestein B, Hill DE, Burrell M;
XX WPI: 1997-153623/14.
XX DR P-PSDB; AAM13380.
XX
XX PT Detection of amplification of human MDM2 gene - useful for diagnosis of
XX neoplasia or potential neoplastic transformation.
XX PS Claim 1; Col 21-24; 35pp; English.
XX
XX CC The present sequence is the human MDM2 cDNA, which was isolated from a
XX human CaCo-2 colonic carcinoma cell cDNA library using a murine MDM2 cDNA
XX probe. The MDM2 cDNA can be used as a probe to detect the amplification
XX or elevated expression of a human MDM2 gene, which is diagnostic of
XX neoplasia or the potential for neoplastic transformation, useful for the
XX detection of, e.g. sarcomas, colorectal carcinoma, lung cancer and
XX chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to correct PF
XX field.)
XX
XX SO Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACCACTCACAAGATTCCA 60
DB |||||||
DB 312 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACCACTCACAAGATTCCA 371
OY 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
```

```
Db 372 GCTTCGGAACAAAGACCCCTGTAGACCAAGCCATCTTTGAAGTATTAAGTCT 431
Qy 121 GTTGTGACAAAAGACACTTATATGAGAAAGGTTCTTTTATCTGGCCAGTAT 180
Db 432 GTTGTGACAAAAGACACTTATATGAGAAAGGTTCTTTTATCTGGCCAGTAT 491
Qy 181 ATTATGACTAAACGATTATATGATGAGAAAGCAACATATTTATTTGTTCAATGAT 240
Db 492 ATTATGACTAAACGATTATATGATGAGAAAGCAACATATTTATTTGTTCAATGAT 551
Qy 241 CTTCTAGAGATTGTTGGCGTGCAGGCTTCTCTGTGAAGACACAGAAATATAT 300
Db 552 CTTCTAGAGATTGTTGGCGTGCAGGCTTCTCTGTGAAGACACAGAAATATAT 611
Qy 301 ACCATGATCTACAGAACTTGTGTAGTCAATCAGACAGAAATCATCGGACTCAGTACA 360
Db 612 ACCATGATCTACAGAACTTGTGTAGTCAATCAGACAGAAATCATCGGACTCAGTACA 671
Qy 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAAGTGGAGTGAT 402
Db 672 TCTGTGAGTGAGAACAGGTGTCACTTGAAAGTGGAGTGAT 713
```

RESULT 15

AAV20549
ID AAV20549 standard; cDNA; 2372 BP.

AC AAV20549;

DT 18-JUN-1998 (first entry)

DE Human MDM2 encoding cDNA.

KW Human, MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma; ss.

XX Homo sapiens.

OS location/Qualifiers

FT 312..1787

FT /*tag a

FT /product= "MDM2"

XX US5736338-A.

XX PD 07-APR-1998.

XX PF 17-FEB-1995; 95US-00390517.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PR 07-APR-1993; 93US-00044619.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;

XX DR WPI; 1998-239206/21.

XX DR P-PSDB; AAW48241.

XX PT Cancer diagnosis - by determination of MDM2 protein.

XX PS Claim 1; Col 21-24; 35pp; English.

XX CC The present sequence encodes human MDM2 (hMDM2) which is used in the
XX CC method of the present invention. The present invention describes a method
XX CC for diagnosing a neoplastic disease caused by overexpression of MDM2
XX CC protein. The method comprises detecting an elevated cellular amount of
XX CC this protein. The method is useful for the diagnosis of sarcoma,
XX CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX CC
XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGTGCAATACCAACATGTCGTGACCTACTGATGCTGTGTAACCACTTCAGATTGCA 60
Db 312 ATGTGCAATACCAACATGTCGTGACCTACTGATGCTGTGTAACCACTTCAGATTGCA 371
Qy 61 GCTTCGGAACAAAGACCCCTGTAGACCAAGCCATGCTTTGAAAGTATTAAGTCT 120
Db 372 GCTTCGGAACAAAGACCCCTGTAGACCAAGCCATGCTTTGAAAGTATTAAGTCT 431
Qy 121 GTTGTGACAAAAGACACTTATATGATGAGAAAGGTTCTTTTATCTGGCCAGTAT 180
Db 432 GTTGTGACAAAAGACACTTATATGATGAGAAAGGTTCTTTTATCTGGCCAGTAT 491
Qy 181 ATTATGACTAAACGATTATATGATGAGAAAGCAACATATTTATTTGTTCAATGAT 240
Db 492 ATTATGACTAAACGATTATATGATGAGAAAGCAACATATTTATTTGTTCAATGAT 551
Qy 241 CTTCTAGAGATTGTTGGCGTGCAGGCTTCTCTGTGAAGACACAGAAATATAT 300
Db 552 CTTCTAGAGATTGTTGGCGTGCAGGCTTCTCTGTGAAGACACAGAAATATAT 611
Qy 301 ACCATGATCTACAGAACTTGTGTAGTCAATCAGACAGAAATCATCGGACTCAGTACA 360
Db 612 ACCATGATCTACAGAACTTGTGTAGTCAATCAGACAGAAATCATCGGACTCAGTACA 671
Qy 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAAGTGGAGTGAT 402
Db 672 TCTGTGAGTGAGAACAGGTGTCACTTGAAAGTGGAGTGAT 713
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Search completed: October 18, 2004, 12:02:27
Job time : 991 secs

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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 402 | 100.0 | 652 | 3 | US-09-510-252-3 |
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| 3 | 402 | 100.0 | 2372 | 1 | US-07-903-103-1 |
| 4 | 402 | 100.0 | 2372 | 1 | US-08-044-619A-1 |
| 5 | 402 | 100.0 | 2372 | 1 | US-08-283-911-1 |
| 6 | 402 | 100.0 | 2372 | 1 | US-08-245-500A-2 |
| 7 | 402 | 100.0 | 2372 | 1 | US-08-390-546-2 |
| 8 | 402 | 100.0 | 2372 | 1 | US-08-390-479A-2 |
| 9 | 402 | 100.0 | 2372 | 1 | US-08-557-393-2 |
| 10 | 402 | 100.0 | 2372 | 1 | US-08-390-516C-2 |
| 11 | 402 | 100.0 | 2372 | 1 | US-08-390-517A-2 |
| 12 | 402 | 100.0 | 2372 | 2 | US-08-390-515A-2 |
| 13 | 402 | 100.0 | 2372 | 2 | US-08-801-718-2 |
| 14 | 402 | 100.0 | 2372 | 3 | US-09-073-567-1 |
| 15 | 402 | 100.0 | 2372 | 3 | US-09-280-805-1 |
| 16 | 402 | 100.0 | 2372 | 3 | US-09-048-810-1 |
| 17 | 402 | 100.0 | 2372 | 3 | US-09-170-159A-2 |
| 18 | 402 | 100.0 | 2372 | 4 | US-09-480-718-3 |
| 19 | 289.2 | 71.9 | 1710 | 1 | US-07-903-103-3 |
| 20 | 289.2 | 71.9 | 1710 | 1 | US-08-044-619A-3 |
| 21 | 289.2 | 71.9 | 1710 | 1 | US-08-283-911-3 |
| 22 | 289.2 | 71.9 | 1710 | 1 | US-08-245-500A-4 |
| 23 | 289.2 | 71.9 | 1710 | 1 | US-08-390-546-4 |
| 24 | 289.2 | 71.9 | 1710 | 1 | US-08-390-479A-4 |
| 25 | 289.2 | 71.9 | 1710 | 1 | US-08-557-393-4 |
| 26 | 289.2 | 71.9 | 1710 | 1 | US-08-390-516C-4 |
| 27 | 289.2 | 71.9 | 1710 | 1 | US-08-390-517A-4 |

| | | | | | | |
|----|-------|------|------|---|--------------------|--------------------|
| 28 | 289.2 | 71.9 | 1710 | 1 | US-08-390-515A-4 | Sequence 4, Appli |
| 29 | 289.2 | 71.9 | 1710 | 2 | US-08-801-718-4 | Sequence 4, Appli |
| 30 | 289.2 | 71.9 | 1710 | 3 | US-09-073-567-12 | Sequence 12, Appli |
| 31 | 289.2 | 71.9 | 1710 | 3 | US-09-170-159A-4 | Sequence 4, Appli |
| 32 | 289.2 | 71.9 | 1710 | 4 | US-09-480-718-45 | Sequence 45, Appli |
| 33 | 289.2 | 56.5 | 309 | 3 | US-09-167-322-9 | Sequence 9, Appli |
| 34 | 160.8 | 40.0 | 966 | 3 | US-09-167-322-7 | Sequence 7, Appli |
| 35 | 131 | 32.6 | 199 | 4 | US-09-200-355-1 | Sequence 1, Appli |
| 36 | 131 | 32.6 | 199 | 4 | US-09-200-355-2 | Sequence 1, Appli |
| 37 | 95.6 | 23.8 | 2192 | 3 | US-09-289-267-1 | Sequence 1, Appli |
| 38 | 88.8 | 22.1 | 399 | 3 | US-09-167-322-8 | Sequence 8, Appli |
| 39 | 82.4 | 20.5 | 891 | 3 | US-09-167-322-5 | Sequence 5, Appli |
| 40 | 82 | 20.4 | 657 | 3 | US-09-167-322-6 | Sequence 6, Appli |
| 41 | 70.8 | 17.6 | 500 | 3 | US-09-280-805-2 | Sequence 2, Appli |
| 42 | 70.8 | 17.6 | 500 | 3 | US-09-048-810-2 | Sequence 2, Appli |
| 43 | 49 | 12.2 | 73 | 3 | US-09-073-567-49 | Sequence 49, Appli |
| 44 | 38.4 | 9.6 | 40 | 3 | US-09-540-599-17 | Sequence 17, Appli |
| 45 | 36.8 | 9.2 | 399 | 4 | US-09-621-976-8976 | Sequence 8976, Ap |

ALIGNMENTS

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RESULT 1
US-09-510-252-3
Sequence 3, Application US/09510252
Patent No. 6372490
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Yang, MeiJia
APPLICANT: Schulz, Vincent
APPLICANT: Curagen Corporation
TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
FILE REFERENCE: 15966-524 MDM US
CURRENT APPLICATION NUMBER: US/09/510,252
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: USSN 60/121,192
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 652
TYPE: DNA
ORGANISM: Homo sapiens
US-09-510-252-3

Query Match      100.0%; Score 402; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 2,3e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGCAATACCAACATGTCGTACTGATGATGTCGTAAACACCTCAGATTCCA 60
DB      1 ATGTGCAATACCAACATGTCGTACTGATGATGTCGTAAACACCTCAGATTCCA 60

QY      61 GCTTCGGAACAGAGACCCCTGCTTAAGCAAGGCAATGCTTTGAAGTATTAAAGTCT 120
DB      61 GCTTCGGAACAGAGACCCCTGCTTAAGCAAGGCAATGCTTTGAAGTATTAAAGTCT 120

QY      121 GTTGGTGCACAAAAGACCTTATCTATGATGAAGAGGTTCTTTTATCTTGGCCAGTAT 180
DB      121 GTTGGTGCACAAAAGACCTTATCTATGATGAAGAGGTTCTTTTATCTTGGCCAGTAT 180

QY      181 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGTAATGTTCAATGAT 240
DB      181 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGTAATGTTCAATGAT 240

QY      241 CTTCTAGAGATTGTTGCGCGCCCAAGCTTCTCTGTGAAGGACACAGAAAATATAT 300
DB      241 CTTCTAGAGATTGTTGCGCGCCCAAGCTTCTCTGTGAAGGACACAGAAAATATAT 300

QY      301 ACATGATCTACAGGAACCTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 360
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Qy 241 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGTGAAAGACACAGAAAAATATAT 300
 Db 552 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGTGAAAGACACAGAAAAATATAT 611
 Qy 301 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 360
 Db 612 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 671
 Qy 361 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGATGAT 402
 Db 672 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGATGAT 713

RESULT 4
 US-08-044-619A-1
 Sequence 1, Application US/0804619A

GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY
 APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
 TITLE OF INVENTION: HUMAN TUMORS
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 STREET: 1001 G ST., N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001-4597
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/044.619A
 FILING DATE: 07-APR-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/903.103
 FILING DATE: 23-JUN-1992
 APPLICATION NUMBER: US 07/867.840
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.40148
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9239
 TELEX: 197430 BBMB UT
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL LINE: Caco-2
 POSITION IN GENOME:
 MAP POSITION: 12q12-14
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 312..1784
 US-08-044-619A-1

Query Match 100.0%; Score 402; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3,5e-103;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGTGCAATACCAACATGTCTGTACCTAGATGCTGCTTAACCACTCAGATTCCA 60
 Db 312 ATGTGCAATACCAACATGTCTGTACCTAGATGCTGCTTAACCACTCAGATTCCA 371
 Qy 61 GCTTCGGAACAGAGACCCCTGTAGACCAAGCCATTGCTTTGAATTAAAGTCT 120
 Db 372 GCTTCGGAACAGAGACCCCTGTAGACCAAGCCATTGCTTTGAATTAAAGTCT 431
 Qy 121 GTTGTGCACAAAAAGACCTTATATGAGAAAGGCTCTTTTATCTTGGCCAGTAT 180
 Db 432 GTTGTGCACAAAAAGACCTTATATGAGAAAGGCTCTTTTATCTTGGCCAGTAT 491
 Qy 181 ATTTGATTAACGATTATATGATGAGAACCAACATATTTGTTCAAAATGAT 240
 Db 492 ATTTGATTAACGATTATATGATGAGAACCAACATATTTGTTCAAAATGAT 551
 Qy 241 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGTGAAAGACACAGAAAAATATAT 300
 Db 552 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGTGAAAGACACAGAAAAATATAT 611
 Qy 301 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 360
 Db 612 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 671
 Qy 361 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGATGAT 402
 Db 672 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGATGAT 713

RESULT 5
 US-08-283-911-1
 Sequence 1, Application US/08283911

GENERAL INFORMATION:
 APPLICANT: VOGELSTEIN, BERT
 APPLICANT: KINZLER, KENNETH
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
 TITLE OF INVENTION: HUMAN TUMORS
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 STREET: 1001 G ST., N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001-4597
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/283.911
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/903.103
 FILING DATE: 23-JUN-1992
 APPLICATION NUMBER: US 07/867.840
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.40148
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9239
 TELEX: 197430 BBMB UT
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,546
FILING DATE: 07-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-546-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCGTACCTAAGTGTGCTGTAACCACTCAGCAATTCCA 60
DB 312 ATGTGCAATACCAACATGTCGTACCTAAGTGTGCTGTAACCACTCAGCAATTCCA 371

QY 61 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 431

QY 121 GTTGTGACAAAAGACACTTATATGATGAAGAGTCTTTTATTCCTGGCAGTAT 180
DB 432 GTTGTGACAAAAGACACTTATATGATGAAGAGTCTTTTATTCCTGGCAGTAT 491

QY 181 ATTATGACTAAAGCATTTATGATGAGAGCAACAATATTGTAATTTGTTCAAAATGAT 240
DB 492 ATTATGACTAAAGCATTTATGATGAGAGCAACAATATTGTAATTTGTTCAAAATGAT 551

QY 241 CTTTAGAGAGATTGTTGGGTCGCAAGCTTCTGTGAAAGAGACAGAAAATATAT 300
DB 552 CTTTAGAGAGATTGTTGGGTCGCAAGCTTCTGTGAAAGAGACAGAAAATATAT 611

QY 301 ACCATGATCTACAGAACTTGTGTAGTAGTCAATGACAGAAATCATGGAATCAGATACA 360
DB 612 ACCATGATCTACAGAACTTGTGTAGTAGTCAATGACAGAAATCATGGAATCAGATACA 671

QY 361 TCTGTGAGTGAGACAGGTGACCTTGAAGTGGAGTGT 402
DB 672 TCTGTGAGTGAGACAGGTGACCTTGAAGTGGAGTGT 713

RESULT 8
US-08-390-479A-2
Sequence 2, Application US/08390479A
Patent No. 5618921
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,479A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-479A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCGTACCTAAGTGTGCTGTAACCACTCAGCAATTCCA 60
DB 312 ATGTGCAATACCAACATGTCGTACCTAAGTGTGCTGTAACCACTCAGCAATTCCA 371

QY 61 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 431

QY 121 GTTGGTCACAAAAACACTTATCTATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
| | | | |
Db 432 GTTGGTCACAAAAAGACACTTATCTATGTAAGAGGTTCTTTTATCTTGCCAGTAT 491
| | | | |
QY 181 ATTATGACTAAAGCATTTATATGATGAGAACAAACATATGATTTGTTCAAAATGAT 240
| | | | |
Db 492 ATTATGACTAAAGCATTTATATGATGAGAACAAACATATGATTTGTTCAAAATGAT 551
| | | | |
QY 241 CTTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGACACAGAAAATATAT 300
| | | | |
Db 552 CTTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGACACAGAAAATATAT 611
| | | | |
QY 301 ACCATGATCTACAGAACTTGTTGTTGATGTCATCAGCAGAAATATGAGTACGATAC 360
| | | | |
Db 612 ACCATGATCTACAGAACTTGTTGTTGATGTCATCAGCAGAAATATGAGTACGATAC 671
| | | | |
QY 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 402
| | | | |
Db 672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 713
| | | | |

RESULT 9

US-08-557-393-2
; Sequence 2, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A. 32,141
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: Caco-2
; POSITION IN GENOME:

MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
US-08-557-393-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATTCACAACTGCTGTACCTACCTGATGAGTGGTGTACCACTCCAGATTTCCA 60
| | | | |
Db 312 ATGTGCAATTCACAACTGCTGTACCTACCTGATGAGTGGTGTACCACTCCAGATTTCCA 371
| | | | |
QY 61 GCTTGGAAACAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAAGTCT 120
| | | | |
Db 372 GCTTGGAAACAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAAGTCT 431
| | | | |
QY 121 GTTGGTCACAAAAACACTTATCTATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
| | | | |
Db 432 GTTGGTCACAAAAACACTTATCTATGTAAGAGGTTCTTTTATCTTGCCAGTAT 491
| | | | |
QY 181 ATTATGACTAAAGCATTTATATGATGAGAACAAACATATGATTTGTTCAAAATGAT 240
| | | | |
Db 492 ATTATGACTAAAGCATTTATATGATGAGAACAAACATATGATTTGTTCAAAATGAT 551
| | | | |
QY 241 CTTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGACACAGAAAATATAT 300
| | | | |
Db 552 CTTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGACACAGAAAATATAT 611
| | | | |
QY 301 ACCATGATCTACAGAACTTGTTGTTGATGTCATCAGCAGAAATATGAGTACGATAC 360
| | | | |
Db 612 ACCATGATCTACAGAACTTGTTGTTGATGTCATCAGCAGAAATATGAGTACGATAC 671
| | | | |
QY 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 402
| | | | |
Db 672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 713
| | | | |

RESULT 10

US-08-390-516C-2
; Sequence 2, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A. 32,141
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-516C-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTTATGATGCTGTACCACTCAAGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACCTTATGATGCTGTACCACTCAAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCTTGTAGACCAAGCATTTCTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCTTGTAGACCAAGCATTTCTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGACACAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGCCAGTAT 180
DB 432 GTTGTGACACAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGCCAGTAT 491
QY 181 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGTAATTTGTTCAATGAT 240
DB 492 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGTAATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGGAACCTTGTAGTCAATCAGCAGAAATCATCGGACTCAGTACA 360
DB 612 ACCATGATCTACAGGAACCTTGTAGTCAATCAGCAGAAATCATCGGACTCAGTACA 671
QY 361 TCTGTGAGTAGAAGCAGGTGTCACTTGAAGTGGAGTAT 402
DB 672 TCTGTGAGTAGAAGCAGGTGTCACTTGAAGTGGAGTAT 713

RESULT 11
US-08-390-517A-2
; Sequence 2, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BEKT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001

US-08-390-515A-2
; Sequence 2, Application US/08390515A
; Patent No. 5756455

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,517A
FILING DATE: 07-Apr-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-517A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTTATGATGCTGTACCACTCAAGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACCTTATGATGCTGTACCACTCAAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCTTGTAGACCAAGCATTTCTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCTTGTAGACCAAGCATTTCTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGACACAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGCCAGTAT 180
DB 432 GTTGTGACACAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGCCAGTAT 491
QY 181 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGTAATTTGTTCAATGAT 240
DB 492 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGTAATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGGAACCTTGTAGTCAATCAGCAGAAATCATCGGACTCAGTACA 360
DB 612 ACCATGATCTACAGGAACCTTGTAGTCAATCAGCAGAAATCATCGGACTCAGTACA 671
QY 361 TCTGTGAGTAGAAGCAGGTGTCACTTGAAGTGGAGTAT 402
DB 672 TCTGTGAGTAGAAGCAGGTGTCACTTGAAGTGGAGTAT 713

RESULT 12
US-08-390-515A-2
; Sequence 2, Application US/08390515A
; Patent No. 5756455

GENERAL INFORMATION:
APPLICANT: BURELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: HUMAN TUMORS
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,515A
FILING DATE: 07-APR-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-515A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No.3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTTACTGATGTGCTGTAACCACTCAGATTTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACTTACTGATGTGCTGTAACCACTCAGATTTCCA 371
QY 61 GCTTGGCAACGAGACCTGTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTGGCAACGAGACCTGTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 431
QY 121 GTTGGTGCACAAAAGACACTTATCTATGATGAAGAGGTTCTTTTATCTTGGCAGTAT 180
DB 432 GTTGGTGCACAAAAGACACTTATCTATGATGAAGAGGTTCTTTTATCTTGGCAGTAT 491
QY 181 ATTATGACTTAACGATTATATGATGAGAAGCAACATATTGATATTGTTCAATGAT 240
DB 492 ATTATGACTTAACGATTATATGATGAGAAGCAACATATTGATATTGTTCAATGAT 551
QY 241 CTTCTAGAGAGATTGTTGGCGTGCAGGCTTCTGTGAAGAGCACAGGAAAATATAT 300

DB 552 CTTCTAGAGAGATTGTTGGCGTGCAGGCTTCTGTGAAGAGCACAGGAAAATATAT 611
QY 301 ACCATGATCTACAGAACTGTAGTATCATCAGAGAAATCATCGACTCAGGTACA 360
DB 612 ACCATGATCTACAGAACTGTAGTATCATCAGAGAAATCATCGACTCAGGTACA 671
QY 361 TCTGTAGTGAAGAACGTTGTCACCTTGAAGGTGGAGTGAT 402
DB 672 TCTGTAGTGAAGAACGTTGTCACCTTGAAGGTGGAGTGAT 713

RESULT 13

US-08-801-718-2
Sequence 2, Application US/08801718
Patent No. 5858976

GENERAL INFORMATION:

APPLICANT: BURELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,718
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-801-718-2

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No.3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGTGCAATACCAACATGCTGTACTGATGTGCTGTAAACCACTCAGAGATTCCA 60
Db 312 ATGTGCAATACCAACATGCTGTACTGATGTGCTGTAAACCACTCAGAGATTCCA 371
Qy 61 GCTTGGAAACAAGACCCCTGTGATGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
Db 372 GCTTGGAAACAAGACCCCTGTGATGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
Qy 121 GTTGTGACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCCAGAT 180
Db 432 GTTGTGACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCCAGAT 491
Qy 181 ATTATGACTAAACGATTATATGATGAGAAACAACATATGATATTTGTTCAATGAT 240
Db 492 ATTATGACTAAACGATTATATGATGAGAAACAACATATGATATTTGTTCAATGAT 551
Qy 241 CTTTAGAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGACACAGAAAATATAT 300
Db 552 CTTTAGAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGACACAGAAAATATAT 611
Qy 301 ACCATGATCTACAGAACTGTGTAGTACATCAGCAAGATCATCGACTCAGATACA 360
Db 612 ACCATGATCTACAGAACTGTGTAGTACATCAGCAAGATCATCGACTCAGATACA 671
Qy 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGTAT 402
Db 672 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGTAT 713

```

RESULT 14
US-09-073-567-1
Sequence 1, Application US/09073567
Patent No. 6013786

```

GENERAL INFORMATION:
APPLICANT: Jiaodong Chen
APPLICANT: Sudhir Agrawal
APPLICANT: Rudhen Zhang
TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073.567
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 98,057-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: hmdm2 DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-073-567-1

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Query Match      100.0%; Score 402; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3,5e-103;
Matches, 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCAATACCAACATGCTGTACTGATGTGCTGTAAACCACTCAGAGATTCCA 60
Db 312 ATGTGCAATACCAACATGCTGTACTGATGTGCTGTAAACCACTCAGAGATTCCA 371
Qy 61 GCTTGGAAACAAGACCCCTGTGATGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
Db 372 GCTTGGAAACAAGACCCCTGTGATGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
Qy 121 GTTGTGACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCCAGAT 180
Db 432 GTTGTGACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCCAGAT 491
Qy 181 ATTATGACTAAACGATTATATGATGAGAAACAACATATGATATTTGTTCAATGAT 240
Db 492 ATTATGACTAAACGATTATATGATGAGAAACAACATATGATATTTGTTCAATGAT 551
Qy 241 CTTTAGAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGACACAGAAAATATAT 300
Db 552 CTTTAGAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGACACAGAAAATATAT 611
Qy 301 ACCATGATCTACAGAACTGTGTAGTACATCAGCAAGATCATCGACTCAGATACA 360
Db 612 ACCATGATCTACAGAACTGTGTAGTACATCAGCAAGATCATCGACTCAGATACA 671
Qy 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGTAT 402
Db 672 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGTAT 713

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RESULT 15

US-09-280-805-1
Sequence 1, Application US/09280805
Patent No. 6184212

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GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESS: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280.805
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/048,810
FILING DATE: March 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: Nucleic Acid

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STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
PUBLICATION INFORMATION:
AUTHORS: Oliner, J.D.
AUTHORS: Kinzler, K.W.
AUTHORS: Meltzer, P.S.
AUTHORS: George, D.L.
AUTHORS: Vogelstein, B.
TITLE: Amplification of a gene encoding a
TITLE: p53-associated protein in human sarcomas
JOURNAL: Nature
VOLUME: 358
ISSUE: 6381
PAGES: 80-83
DATE: 02-JUL-1992
US-09-280-805-1

Query Match 100.0%; Score 402; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTTACTGATGTGCTGTAAACCACCTCAGAGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACCTTACTGATGTGCTGTAAACCACCTCAGAGATTCCA 371
QY 61 GCTTCGGAACAGAGACCTGTGTAGACCAAAAGCATTGCTTTGAAGTTATTAAAGTCT 120
DB 372 GCTTCGGAACAGAGACCTGTGTAGACCAAAAGCATTGCTTTGAAGTTATTAAAGTCT 431
QY 121 GTTGTGCACAAAAGACACTTATATATGAAAGAGGTTCTTTTATCTTGCCAGTAT 180
DB 432 GTTGTGCACAAAAGACACTTATATATGAAAGAGGTTCTTTTATCTTGCCAGTAT 491
QY 181 ATTTATGCTAAACGATTATATGATGAGAGCAACAATATGTTATTTGTTCAATGAT 240
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QY 241 CTTCTAGGAGATTGTTGGCGTSCCAAGCTTCTCTGTGAAAAGACAAGGAAATATAT 300
DB 552 CTTCTAGGAGATTGTTGGCGTSCCAAGCTTCTCTGTGAAAAGACAAGGAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTAGTATCATCAGCAGAGAAATCATCGAATCAGGTACA 360
DB 612 ACCATGATCTACAGAACTTGTAGTATCATCAGCAGAGAAATCATCGAATCAGGTACA 671
QY 361 TCTGTGAGTGAACAGGTGTCACTTGAAGTGGAGTGAAT 402
DB 672 TCTGTGAGTGAACAGGTGTCACTTGAAGTGGAGTGAAT 713

Search completed: October 18, 2004, 14:58:20
Job time : 377 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: October 18, 2004, 11:45:45 : Search time 7330 Seconds
(without alignments)
1998.468 Million cell updates/sec

Title: US-10-724-225-1_COPY_1_402

Perfect score: 402
Sequence: 1 ATGCGAATACCAACATGTC.....ACCTGAAGTGGAGTGAT 402

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g861:*
9: gb_g862:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 402 | 100.0 | 970 | 4 | BM479400 AGENCOURT |
| 2 | 401 | 99.8 | 709 | 2 | BF057574 7K46C07.X |
| 3 | 394.6 | 98.2 | 739 | 7 | CR629819 DKF2p469A |
| 4 | 373.4 | 92.9 | 482 | 7 | R80343 |
| 5 | 366.8 | 91.2 | 779 | 7 | CO737650 SLH03C18 |
| 6 | 366.8 | 91.2 | 858 | 7 | CO737954 SLH03C19 |
| 7 | 353 | 87.8 | 778 | 2 | BE900427 601673652 |
| 8 | 347.6 | 86.5 | 728 | 7 | CO738288 SLE04C20 |
| 9 | 324.4 | 80.7 | 345 | 2 | BE765314 IL2-NT010 |
| 10 | 324 | 80.6 | 393 | 1 | AL704062 DKF2p686N |
| 11 | 318 | 79.1 | 518 | 1 | AL902188 IL-BT002 |
| 12 | 310 | 77.1 | 400 | 7 | CN409877 170004182 |
| 13 | 297.4 | 74.0 | 1008 | 2 | BF683210 602139223 |
| 14 | 294.6 | 73.3 | 507 | 2 | BF114786 7J67d06.X |
| 15 | 294.6 | 73.3 | 512 | 2 | BF435134 |
| 16 | 289.8 | 72.1 | 556 | 2 | BF548539 UI-R-A0-a |
| 17 | 289.8 | 72.1 | 774 | 7 | CK469133 AGENCOURT |
| 18 | 289.8 | 72.1 | 815 | 7 | CK469134 AGENCOURT |
| 19 | 289.8 | 72.1 | 822 | 7 | CK598265 AGENCOURT |
| 20 | 289.8 | 72.1 | 836 | 7 | CK653033 AGENCOURT |
| 21 | 289.8 | 72.1 | 845 | 7 | CK470726 AGENCOURT |
| 22 | 289.2 | 71.9 | 468 | 6 | CD549480 B0299B01- |
| 23 | 289.2 | 71.9 | 468 | 6 | CD562678 B0451D06- |
| 24 | 289.2 | 71.9 | 524 | 6 | CA871480 K0910F02- |

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| 25 | 289.2 | 71.9 | 524 | 7 | CN684573 | CN684573 E0195B12- |
| 26 | 289.2 | 71.9 | 602 | 6 | CA890782 | CA890782 B0161B05- |
| 27 | 289.2 | 71.9 | 612 | 6 | CA890706 | CA890706 B0161A01- |
| 28 | 289.2 | 71.9 | 638 | 7 | CF903758 | CF903758 A0413B01- |
| 29 | 289.2 | 71.9 | 642 | 6 | BY743471 | BY743471 BY743471 |
| 30 | 289.2 | 71.9 | 663 | 6 | BY745235 | BY745235 BY745235 |
| 31 | 289.2 | 71.9 | 669 | 6 | BY754572 | BY754572 BY754572 |
| 32 | 289.2 | 71.9 | 687 | 5 | B0571946 | B0571946 UI-M-FCO- |
| 33 | 289.2 | 71.9 | 754 | 5 | B0708267 | B0708267 UI-M-FCO- |
| 34 | 289.2 | 71.9 | 2999 | 3 | AK088638 | AK088638 MUS muscu |
| 35 | 289.2 | 71.9 | 3007 | 3 | AK004881 | AK004881 MUS muscu |
| 36 | 289.2 | 71.9 | 3028 | 3 | AK004719 | AK004719 MUS muscu |
| 37 | 288.2 | 71.7 | 650 | 6 | BY743294 | BY743294 BY743294 |
| 38 | 287.8 | 71.6 | 476 | 2 | BE676440 | BE676440 7E29h02.X |
| 39 | 287.6 | 71.5 | 477 | 2 | CN677189 | CN677189 A0992F03- |
| 40 | 287.6 | 71.5 | 486 | 7 | CN700295 | CN700295 E0433B09- |
| 41 | 287.6 | 71.5 | 604 | 7 | CN702182 | CN702182 E0459A08- |
| 42 | 287.6 | 71.5 | 617 | 2 | AM822859 | AM822859 UG21A07.Y |
| 43 | 287.6 | 71.5 | 664 | 2 | BE300019 | BE300019 G00944138 |
| 44 | 286 | 71.1 | 663 | 6 | BY746837 | BY746837 BY746837 |
| 45 | 286 | 71.1 | 669 | 2 | AW231125 | AW231125 u039h02.Y |

ALIGNMENTS

RESULT 1
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LOCUS AGENCOURT 6418503 NIH_MGC_67 Homo sapiens CDNA IMAGE:5502336
DEFINITION 5', mRNA sequence.
ACCESSION BM479400.1 GI:18528442
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNLN12140 row: 6 column: 01
High quality sequence stop: 597.
Location/Qualifiers

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/clone="IMAGE:5502336"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 100.0%; Score 402; DB 4; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.7e-101; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0;
1 ATGCGAATACCAACATGCTGACCTACCTAGATGCTGCTAACCACTACAGATTCCA 60


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Qy 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 300
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Qy 301 ACCATGATCTACAGAACTTGTAGTACATCAGAGATCATCGACTCAGTACA 360
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Db 376 ACCATGATCTACAGAACTTGTAGTACATCAGAGATCATCGACTCAGTACA 435
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Qy 361 TCTGTAGTGAAGAACAGGTGTACCTTGAAGGTGGAGTAT 402
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Db 436 TCTGTAGTGAAGAACAGGTGTACCTTGAAGGTGGAGTAT 477

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ACCESSION
BF057574
VERSION
BF057574.1 GI:10811470
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 709)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Straubeberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 481.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3478285"
/tissue_type="fibroheoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NCI_CGAP_OV18"
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGAGGAGCGCGGCAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3478285"
/tissue_type="fibroheoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NCI_CGAP_OV18"
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGAGGAGCGCGGCAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library

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ORIGIN

went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match 99.8%; Score 401; DB 2; Length 709;
 Best Local Similarity 99.8%; Pred. No. 6, 5e-101;
 Matches 401; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ATGCAATACCAACATGTCTGTACTGATGCTGTGTAACCACTCAGATTCCA 60
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Db 206 ATGCAATACCAACATGTCTGTACTGATGCTGTGTAACCACTCAGATTCCA 255
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Qy 61 GCTTCGGAACAGAGACCCCTGTAGACCAAGCATCTCTTGAAGTATTAATCT 120
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Db 266 GCTTCGGAACAGAGACCCCTGTAGACCAAGCATCTCTTGAAGTATTAATCT 325
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Qy 121 GTTGTGCACAAAAGACCTTATCTATGAGAGAGGTTCTTTTATCTTGGCAGTAT 180
|||
Db 326 GTTGTGCACAAAAGACCTTATCTATGAGAGAGGTTCTTTTATCTTGGCAGTAT 385
|||
Qy 181 ATTATGACTAAAGCATTTATGATGAGAGCAACATATTGTATTTGTTCAATGAT 240
|||
Db 386 ATTATGACTAAAGCATTTATGATGAGAGCAACATATTGTATTTGTTCAATGAT 445
|||
Qy 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 300
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Db 446 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 505
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Qy 301 ACCATGATCTACAGAACTTGTAGTACATCAGAGATCATCGACTCAGTACA 360
|||
Db 506 ACCATGATCTACAGAACTTGTAGTACATCAGAGATCATCGACTCAGTACA 565
|||
Qy 361 TCTGTAGTGAAGAACAGGTGTACCTTGAAGGTGGAGTAT 402
|||
Db 566 TCTGTAGTGAAGAACAGGTGTACCTTGAAGGTGGAGTAT 607

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RESULT 3
CR629819 739 bp mRNA linear EST 11-AUG-2004
DEFINITION
DKFZp469A1622_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
ACCESSION
CR629819
VERSION
CR629819.1 GI:51125899
KEYWORDS
EST.
SOURCE
Pongo pygmaeus (orangutan)
ORGANISM
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
REFERENCE
1 (bases 1 to 739)
Bahar, A., Lauber, J., Mewes, H.W., Weill, B., Amdt, C., Oeinger, A.,
Rohde, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Bahar, A., Lauber, J., Mewes, H.W., et al.)
Unpublished (2004)
Contact: MIPS
TITLE
Pongo pygmaeus mRNA (Bahar, A., Lauber, J., Mewes, H.W., et al.)
JOURNAL
COMMENT
Contact: MIPS

```

Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email: s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
 (Hilden, Germany) within the cDNA sequencing consortium of the
 German Genome Project. This clone (DKFZp469A1622) is available at
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
 Berlin, Germany. Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp469A1622
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

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FEATURES
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/db_xref="taxon:9600"
/clone="DKFZp469A1622"

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TITLE
Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, *Spermophilus lateralis*
Unpublished (2004)
JOURNAL
COMMENT
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 18 row: d column: 24
Seq primer: pf1c T7 (5'-AATACGACTCACTATAGG-3')
High quality sequence stop: 779.
Location/Qualifiers

FEATURES

source

1..779
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/mol_type="mRNA"
/db_xref="taxon:76772"
/clone="18d24"
/sex="Male & female"
/tissue_type="Heart"
/dev_stage="Adult"
/lab_host="E.coli Electromax DH10B"
/clone_1b="squirrel heart library 1"
/note="Vector: pFLC; Site 1: SalI GTCGAG; Site 2: BamHI
GATCC; Normalized and subcloned cDNA library prepared
from heart of hibernating and summer animals"

ORIGIN

Query Match

Best Local Similarity 91.2%; Score 366.8; DB 7; Length 779;
Pred. No. 2.3e-91;
Matches 380; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACACCTCAGATTCCA 60
DB 125 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACACCTCAGATTCCA 184
QY 61 GCTTCGGAACAGAGACCTGCTTGAACCAAGCCATGCTTTGAAATTAATTAATCT 120
DB 185 GCTTCGGAACAGAGACCTGCTTGAACCAAGCCATGCTTTGAAATTAATTAATCT 244
QY 121 GTTGTGACAAAAAGACCTTATCTATGAAAAGAGTCTTTTATCTTGGCCAGTAT 180
DB 245 GTTGTGACAAAAAGACCTTATCTATGAAAAGAGTCTTTTATCTTGGCCAGTAT 304
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTAATGTTCAATGAT 240
DB 305 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTAATGTTCAATGAT 364
QY 241 CTTCTGAGAGATTGTTGGCGTGCACAGCTTCTCTGTGAAAAGACAGAAAATTTAT 300
DB 365 CTTCTGAGAGATTGTTGGCGTGCACAGCTTCTCTGTGAAAAGACAGAAAATTTAT 424
QY 301 ACCATGATCTACAGAACTTGTAGTATGATCAATCAGAGAAATCATGAGTACATCA 360
DB 425 ACATGATCTACAAAAATTTGGTGTAGTCAATCAGAGAAACATAGATTCACAGACA 484
QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 402
DB 485 TTAGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 526

RESULT 6
COT37954 858 bp mRNA linear EST 29-JUN-2004
LOCUS
DEFINITION
SILH03c19b19f1 squirrel heart library 1 *Spermophilus lateralis* cDNA
clone 19b19 5', mRNA sequence.
ACCESSION
COT37954
VERSION
COT37954.1 GI:50825224
KEYWORDS
Spermophilus lateralis (golden-mantled ground squirrel)

ORGANISM
Spermophilus lateralis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
Spermophilus.
1 (bases 1 to 858)
REFERENCE
AUTHORS
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Rogers, J., and Cossins, A.R.
TITLE
Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, *Spermophilus lateralis*
Unpublished (2004)
JOURNAL
COMMENT
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 19 row: b column: 19
Seq primer: pf1c T7 (5'-AATACGACTCACTATAGG-3')
High quality sequence stop: 858.
Location/Qualifiers

FEATURES

source

1..858
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/mol_type="mRNA"
/db_xref="taxon:76772"
/clone="19b19"
/sex="Male & female"
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/dev_stage="Adult"
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/clone_1b="squirrel heart library 1"
/note="Vector: pFLC; Site 1: SalI GTCGAG; Site 2: BamHI
GATCC; Normalized and subcloned cDNA library prepared
from heart of hibernating and summer animals"

ORIGIN

Query Match

Best Local Similarity 91.2%; Score 366.8; DB 7; Length 858;
Pred. No. 2.4e-91;
Matches 380; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACACCTCAGATTCCA 60
DB 160 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACACCTCAGATTCCA 219
QY 61 GCTTCGGAACAGAGACCTGCTTGAACCAAGCCATGCTTTGAAATTAATTAATCT 120
DB 220 GCTTCGGAACAGAGACCTGCTTGAACCAAGCCATGCTTTGAAATTAATTAATCT 279
QY 121 GTTGTGACAAAAAGACCTTATCTATGAAAAGAGTCTTTTATCTTGGCCAGTAT 180
DB 280 GTTGTGACAAAAAGACCTTATCTATGAAAAGAGTCTTTTATCTTGGCCAGTAT 339
QY 280 GTTGTGACAAAAAGACCTTATCTATGAAAAGAGTCTTTTATCTTGGCCAGTAT 339
DB 340 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTAATGTTCAATGAT 399
QY 340 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGTAATGTTCAATGAT 459
DB 400 CTTCTGAGAGATTGTTGGCGTGCACAGCTTCTCTGTGAAAAGACAGAAAATTTAT 459
QY 400 CTTCTGAGAGATTGTTGGCGTGCACAGCTTCTCTGTGAAAAGACAGAAAATTTAT 459
DB 460 ACATGATCTACAAAAATTTGGTGTAGTCAATCAGAGAAACATAGATTCACAGACA 519
QY 460 ACATGATCTACAAAAATTTGGTGTAGTCAATCAGAGAAACATAGATTCACAGACA 519
DB 520 TTAGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 561

RESULT 7
BE900427

LOCUS BE900427 778 bp mRNA linear EST 29-SEP-2000
DEFINITION 601673652F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956413 5',
mRNA sequence.
ACCESSION BE900427
VERSION BE900427.1 GI:10388579
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS NIH-MGC htp://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov
Plate: L1CM832 row: h column: 14
High quality sequence stop: 708.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source

Query Match 87.8%; Score 353; DB 2; Length 778;
Best Local Similarity 96.8%; Pred. No. 1.7e-87;
Matches 392; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

ORIGIN

1 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGTACACCTCACAAGATTGCA 60
288 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGTACACCTCACAAGATTGCA 347
61 GCTTCGGAACAAGAGACCTGCTTACGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
348 GCTTCGGAACAAGAGACCTGCTTACGACCAAGCCATTGCTTTGAAGTTAAAGTCT 407
121 GTTGTGCACAAAAAGACATTATATCTATGAAAGGTTCTTTTATCTTGGCAGAT 180
408 GTTGTGCACAAAAAGACATTATATCTATGAAAGGTTCTTTTATCTTGGCAGAT 467
181 ATTAGCACTAAGCAATATATGATGAGAAACAACATATTTGATATTTCAATATGAT 240
468 ATTAGCACTAAGCAATATATGATGAGAAACAACATATTTGATATTTCAATATGAT 527
241 CTCTAGAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 299
528 CTCTAGAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 587
300 TACATAG-ATCTAGAGAACTTGTGAGTATGTC-AATGCGAGGAATCATCGGACTCGGT 357
588 TACATAGCATCTACAGAACTTGTGAGTATGTC-AATGCGAGGAATCATCGGACTCGGT 647
358 ACATCTGATGAGAGAGGTCACCTTGAAGTGGAGATGAT 402
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Db 648 ACATCTGATGAGAGAGGTCACCTTGAAGTGGAGATGAT 692

RESULT 8
LOCUS CO738288
DEFINITION SILE04c20a14f1 squirrel embryo library 1 Spermophilus lateralis
cDNA clone 20a14 5', mRNA sequence.
ACCESSION CO738288
VERSION CO738288.1 GI:50825558
KEYWORDS EST.
SOURCE Spermophilus lateralis (golden-mantled ground squirrel)
ORGANISM Spermophilus lateralis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Spermophilus.

REFERENCE 1 (bases 1 to 728)
AUTHORS Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Rogers, J. and Cousins, A.R.
TITLE Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
JOURNAL Contact: Andrew R. Cousins
COMMENT Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cousins@lly.ac.uk
Vector has been trimmed from this EST.
Plate: 20 row: a column: 14
Seq primer: p1c 77 (5'-ATTAGCCTCACTAAGG-3')

High quality sequence stop: 728.
Location/Qualifiers
1..728
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/note="Vector: pFLC; Site:1: SalI GTCGAG; Site:2: BamHI
GATCC; Normalized and subcloned cDNA library prepared
from embryos"

FEATURES

source

Query Match 86.5%; Score 347.6; DB 7; Length 728;
Best Local Similarity 93.8%; Pred. No. 5.3e-86;
Matches 362; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

ORIGIN

1 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGTACACCTCACAAGATTGCA 60
343 ATGTGCAATACCAATGCTGTGACCTACTGATGGTGTACACCTCACAAGATTGCA 402
61 GCTTCGGAACAAGAGACCTGCTTACGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
403 GCTTCGGAACAAGAGACCTGCTTACGACCAAGCCATTGCTTTGAAGTTAAAGTCT 462
121 GTTGTGCACAAAAAGACATTATATCTATGAAAGGTTCTTTTATCTTGGCAGAT 180
463 GTTGTGCACAAAAAGACATTATATCTATGAAAGGTTCTTTTATCTTGGCAGAT 522
181 ATTAGCACTAAGCAATATATGATGAGAAACAACATATTTGATATTTCAATATGAT 240
523 ATTAGCACTAAGCAATATATGATGAGAAACAACATATTTGATATTTCAATATGAT 582
241 CTCTAGAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 300
583 CTCTAGAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 642
|||||

| | | | | |
|------------|---|-------------|---|------------------------|
| OY | | 301 | ACCAATGACTCTCAGGAACCTTGTTGTGTACTCATCATGCAGGAAATATCGATCCACGGTACA | 360 |
| Dd | | 643 | ACAATGACTCTCACAAAATTGTTGTGTACTCATCATGCAGGAAACCATCAGATTCACGACACA | 702 |
| OY | | 361 | TCTGTGAGTGAGAACAGGCTGTCACTT | 386 |
| Dd | | 703 | TTAGTAGTGAGAACAGGCTGCCACTT | 728 |
| RESULT 9 | | | | |
| BE765314 | | | | |
| LOCUS | BE765314 | 345 bp | mRNA | linear EST 19-SEP-2000 |
| DEFINITION | IL2-NT0102-280700-115-H11 NT0102 Homo sapiens CDNA, mRNA sequence. | | | |
| ACCESSION | BE765314 | | | |
| VERSION | BE765314.1 | GI:10195238 | | |
| KEYWORDS | EST. | | | |
| SOURCE | Homo sapiens (human) | | | |
| ORGANISM | Homo sapiens | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| | 1 (bases 1 to 345) | | | |
| REFERENCE | Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., | | | |
| AUTHORS | Nagai,M.A., da Silva,W.U.Jr., Zago,M.A., Bordin,S., Costa,F.F., | | | |
| | Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., | | | |
| | Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., | | | |
| | O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and | | | |
| | Simpson,A.J. | | | |
| TITLE | Shotgun sequencing of the human transcriptome with ORF expressed | | | |
| | sequence tags | | | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. | 97 (7), | 3491-3496 | (2000) |
| MEDLINE | 20202663 | | | |
| PUBMED | 10737800 | | | |
| COMMENT | Contact: Simpson A.J.G. | | | |

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/getchem12.pl?tl1=ct2-11L2-NT0102-280>
 700-115-H1&f3=2000-07-28&t4=1)
 Seq primer: puc 18 Forward
 High quality sequence start: 14
 High quality sequence stop: 344.
 Location/Qualifiers
 1..345

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/clone_1db="NT0102"
/note="Organ: nervous tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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| Query Match | 80.7% | Score 324.4 | DB 2 | Length 345 |
|-----------------------|----------------|---|----------|------------|
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| Matches 328 | Conservative 0 | Mismatches 6 | Indels 0 | Gaps 0 |
| Qy | 1 | ATGTGCATATCCAAATGTCTGTACTACTACTATGTCGTGAACCACTCAGACATTCCA | 60 | |
| | | | | |
| Db | 12 | AGGTGCATATCCAAATGTCTGTACTACTACTATGTCGTGAACCACTCAGACATTCCA | 71 | |
| Qy | 61 | GCTTGGCAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTAATTAAGTCT | 120 | |

| | | | |
|----|-----|--|-----|
| Db | 72 | GCTTGGAAACAAGAGACCCCTGGTTATGACCAAGCATTGCTTTTGAAGATATTAAAGTCT | 131 |
| Qy | 121 | GTTGTGACACAAAAGAAGACCTTATACATATGAAAGAGTCTTTTATACCTGGCCAGAT | 180 |
| Db | 132 | GCTGATGACACAAAAGACACTTATACATATGAAAGAGGATCTTTTATCTTGGCCAGTAT | 191 |
| Qy | 181 | ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTATATTGTTCAATAT | 240 |
| Db | 192 | ATTATGACTAAACATTTATATGATGAGAGCAACAACATATTGAATATTGTTCAATAT | 251 |
| Qy | 241 | CTTCTAGAGAGTTTGTGTTGGCGTGCACAGTTCTCTGTGAAAGAGCAGCAAGAAAATATAT | 300 |
| Db | 252 | CTTCTAGAGAGTTTGTGTTGGCGTGCACAGCTTCTCTGTGAAAGAGCAGCAAGAAAATATAT | 311 |
| Qy | 301 | ACCATGATCTACAGGAAGTTGGTATGTGCATC | 334 |
| Db | 312 | ACCATGATCTACAGGAAGTTGGTATGTGCATC | 345 |

| | |
|------------|---|
| RESULT | 10 |
| LOCUS | AL704062 |
| DEFINITION | AL704062 393 bp mRNA linear EST 04-SEP-2001 |
| ACCESSION | DKZPE86N1428.r1.686 (synonym: hlc3) Homo sapiens cDNA clone |
| VERSION | AL704062 |
| KEYWORDS | AL704062.1 GI:19687417 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 393) Ottewaalder,B., Mewes,W., Mewes,H.W., Well,B. and Wiemann,S. EST (Ottewaalder,B., Obermaler,B., Mewes,H.W., Well,B. and Wiemann,S.) Unpublished (2001) Contact: MIPS |
| JOURNAL | |
| COMMENT | |

```

FEATURES
    source
        MIPs
        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
        This is the 5' sequence of the clone insert
        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
        Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
        sequenced by Medigenomix (Martinsried/Germany) within the cDNA
        sequencing consortium of the German Genome Project. No 81 sequence
        available.
        This clone (DKFZp666N1428) is available at the RZPD in Berlin.
        Please contact the RZPD: Ressourcencentrum, Heubnerweg 6, 14059
        Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.
        Location/Qualifiers
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                cDNA collection"
    
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| ORIGIN | Query Match | 80.6% | Score 324 | DB 1 | Length 393 |
|--------|--|----------------|-------------------|----------|------------|
| | Best Local Similarity | 99.4% | Pred. No. 1.8e-79 | | |
| | Matches 324 | Conservative 0 | Mismatches 2 | Indels 0 | Gaps 0 |
| Qy | 1 ATGTGCATATCAACATGTCTGTATCTACTACTGATGTGCTGTAAACACCTCAGATTCCA | | | | 60 |
| Db | 68 ATGTGCATATCAACATGTCTGTATCTACTACTGATGTGCTGTAAACACCTCAGATTCCA | | | | 127 |
| Qy | 61 GCTTGGAAACAGAGACCTGTGCTTAAAGCAACCAATTCCTTTGAAATTAAAGTCT | | | | 120 |

Db 128 GCTTCGGAACAGAGACCCTGGTTAGACAAAGCCATTGCTTTGAAATTATTAAGTCT 187
Qy 121 GTTGTGACACAAAGACCTTATATATGAAGAGTTCTTTTATCTTGGCAGAT 180
Db 188 GNNGTGCACAAAAGACCTTATATATGAAGAGGTTCTTTTATCTTGGCAGAT 247
Qy 181 ATTATGACTAAACGATTATATATGATAGAGCAACACATATTGTATATTTGCAATGAT 240
Db 248 ATTATGACTAAACGATTATATATGATAGAGCAACACATATTGTATATTTGCAATGAT 307
Qy 241 CTCTAGAGATTGTTGTCGTCGCAAGCTTCTCTGTGAAAAGCAGGAAAATATAT 300
Db 308 CTCTAGAGATTGTTGTCGTCGCAAGCTTCTCTGTGAAAAGCAGGAAAATATAT 367
Qy 301 ACCATGATCTACAGGAACCTTGATCT 326
Db 368 ACCATGATCTACAGGAACCTTGATCT 393

RESULT 11
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LOCUS AI902188 11-BT002-221198-015 BT002 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI902188
VERSION AI902188.1 GI:6492666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 518)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordoli, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsuoka, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

TITLE Contact: Simpson A.J.G.
JOURNAL Laboratory of Cancer Genetics
MEDLINE Ludwig Institute for Cancer Research
PUBMED Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
COMMENT Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?i=11&t=IL-BT002-015.html
&t3=221198&t4=1)
Seq primer: puc 18 forward.
FEATURES
Location/Qualifiers
1..518
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_id="BT002"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 79.1%; Score 318; DB 1; Length 518;

Best Local Similarity 89.9%; Pred. No. 9e-78;
Matches 358; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
Qy 5 GCATTAACCAACATCTCTGTAACCTACTGATGCTGTGTAACCACTCAGATTCAGCTT 64
Db 480 GCCATCCCAAAAGGTTGNCNCCTACTGAAAGGCTCGAACCACTTCAGATTCAGCTT 421
Qy 65 CGGAACAAGAGACCCCTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGCTGTG 124
Db 420 GGAACCAAGAGCCCTGTTAGACCAAGCATTGCTTTGAAGTTATTAAGCTGTG 362
Qy 125 GTGCACAAAAGACACTTATATGATAGAGCAACACATATTGTATATTTGCAATGATCTTC 184
Db 361 GTGCNC-AAAAGCATTATATGATAGAGCAACACATATTGTATATTTGCAATGATCTTC 303
Qy 185 TGACTAAAGATTATATGATAGAGCAACACATATTGTATATTTGCAATGATCTTC 244
Db 302 TGACTAAAGATTATATGATAGAGCAACACATATTGTATATTTGCAATGATCTTC 243
Qy 245 TAGAGATTGTTGTCGTCGCAAGCTTCTGTGAAAAGCAGGAAAATATATATCA 304
Db 242 TAGAGATTGTTGTCGTCGCAAGCTTCTGTGAAAAGCAGGAAAATATATATCA 183
Qy 305 TGAATCTACAGAACTTGTAGTATGATCAATGAGCAGAAATCATCGACTCAGTATCTG 364
Db 182 TGATCTACAGAACTTGTAGTATGATCAATGAGCAGAAATCATCGACTCAGTATCTG 123
Qy 365 TGAATGAGAAACAGGTGTACCTTGAAAGTGGAGTAT 402
Db 122 TGAATGAGAAACAGGTGTACCTTGAAAGTGGAGTAT 85

RESULT 12
CN409877 400 bp mRNA linear EST 16-MAY-2004
LOCUS CN409877 17000418214393 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409877
VERSION CN409877.1 GI:47397001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 400)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guebler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 400 Std Error: 0.00.
FEATURES
Location/Qualifiers
1..400
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_id="GRN_EB"
/note="Toigo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 77.1%; Score 310; DB 7; Length 400;

Best Local Similarity 99.7%; Pred. No. 1.5e-75;
Matches 321; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 81 GGTAGACCAAGCATTTGCTTTGAAAGTATTAAGTCTGGTGCACAAAAGAC 140
|||
Db 2 GGTAGACCAAGCC-TTGCTTTGAAAGTATTAAGTCTGGTGCACAAAAGAC 60
|||

QY 141 TTATACATGAAAAGGTTCTTTTATCTTGGCCAGTATATTAAGCATTTA 200
|||
Db 61 TTATACATGAAAAGGTTCTTTTATCTTGGCCAGTATATTAAGCATTTA 120
|||

QY 201 TGAATGAGAACCAACATATTTGATATTTGTTCAATGATCTTACAGAAATTTGTTGG 260
|||
Db 121 TGAATGAGAACCAACATATTTGATATTTGTTCAATGATCTTACAGAAATTTGTTGG 180
|||

QY 261 CGGCAAGCTTCTCTGTGAAAGACACAGAAAATATATACATGATCTACAGAACT 320
|||
Db 181 CGGCAAGCTTCTCTGTGAAAGACACAGAAAATATATACATGATCTACAGAACT 240
|||

QY 321 GGTAGATGCAATCAGACGAATCATCGACATCGTGTGAGTGAAGACAGGTG 380
|||
Db 241 GGTAGATGCAATCAGACGAATCATCGACATCGTGTGAGTGAAGACAGGTG 300
|||

QY 381 TCACCTTGAAGGTGGAGTAT 402
|||
Db 301 TCACCTTGAAGGTGGAGTAT 322
|||

RESULT 13
BF683210 1008 bp mRNA linear EST 22-DEC-2000
LOCUS 602139223F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298285 5',
DEFINITION mRNA sequence.
ACCESSION BF683210 GI:11968618
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1008)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM153 row: m column: 06
High quality sequence stop: 697.
Location/Qualifiers
1. 1008
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4298285"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 74.0%; Score 297.4; DB 2; Length 1008;
Best Local Similarity 81.0%; Pred. No. 5.8e-72;
Matches 401; Conservative 0; Mismatches 1; Indels 93; Gaps 1;

QY 1 ATGTGCAATTCACCAATGCTGTGTAAGTCTGATGCTGCTGTAACCACTCAGATTCCA 60
|||
Db 56 ATGTGCAATTCACCAATGCTGTGTAAGTCTGATGCTGCTGTAACCACTCAGATTCCA 115
|||

QY 61 GCTTGGGCAAGAGAGCCCTGGTTAGACCAAGCCATTCCTTTGAAGTATTAAGTCT 120
|||
Db 116 GCTTGGGCAAGAGAGCCCTGGTTAGACCAAGCCATTCCTTTGAAGTATTAAGTCT 175
|||

QY 121 GTTGTGCAAAAAAAGACATTTACTATGAAG----- 154
|||
Db 176 GTTGTGCAAAAAAAGACATTTACTATGAAGAGATGAGATTCACTATGTTGCC 235
|||

QY 155 ----- 154
|||

Db 236 AGGCTGCTGGAATCTGGGCTCAAGGATCTGCTACCTCGGCTCCTAAAGTCTA 295
|||

QY 155 -----AGTCTTTTATATCTGGCCAGTATATTAAGTAAAGATTATGATGAG 207
|||
Db 296 GATTACAGGTTCTTTTATATCTGGCCAGTATATTAAGTAAAGATTATGATGAG 355
|||

QY 208 AAGCAACAACATATTTGATATTTGTTCAATGATCTTCTAGAGATTGTTGGCGTCCA 267
|||
Db 356 AAGCAACAACATATTTGATATTTGTTCAATGATCTTCTAGAGATTGTTGGCGTCCA 415
|||

QY 268 AGCTTCTGTGGAAGAGACACAGAAAATATATATCATGATCTTACAGAACTTGTAGTA 327
|||
Db 416 AGCTTCTGTGGAAGAGACACAGAAAATATATATCATGATCTTACAGAACTTGTAGTA 475
|||

QY 328 GTCAATCAGACGAATCATCGACATCGTGTGAGTGAAGACAGGTGTCACCTT 387
|||
Db 476 GTCAATCAGACGAATCATCGACATCGTGTGAGTGAAGACAGGTGTCACCTT 535
|||

QY 388 GAAGGTGGAGTAT 402
|||
Db 536 GAAGGTGGAGTAT 550
|||

RESULT 14
BF114786 507 bp mRNA linear EST 24-OCT-2000
LOCUS BF114786
DEFINITION 7567806.x1 Soares NSF Pg 9W OT PA P S1 Homo sapiens cDNA clone
IMAGE:3391499 3' similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ;,
mRNA sequence.
ACCESSION BF114786 GI:10984262
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 507)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from G1bco
High quality sequence stop: 474.
Location/Qualifiers
1. 507
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3391499"

/lab_host="DH10B"
/clone_l1b="Soares NSF P8 9W OT PA P S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HP8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 507;
Best Local Similarity 95.6%; Pred. No. 3.1e-71;
Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACACCTCAGATTCCA 60
DB 185 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACACCTCAGATTCCA 244
QY 61 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 245 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 304
QY 121 GTTGTGACAAAAGACACTTATCTATGAAGAGTCTTTTATCTTGGCAGATAT 180
DB 305 GTTGTGACAAAAGACACTTATCTATGAAGAGTCTTTTATCTTGGCAGATAT 364
QY 181 ATTATGACTAAGCATTTATGATGAGAGCAACATATTGTATTTGTTCAATGAT 240
DB 365 ATTATGACTAAGCATTTATGATGAGAGCAACATATTGTATTTGTTCAATGAT 424
QY 241 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGAGCAGAGAAAATATAT 300
DB 425 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGAGCAGAGTAATCTTC 484
QY 301 ACCATGATCTACAGGAA 317
DB 485 AGTTAGTCCATTGTAA 501

RESULT 15

BP435134 512 bp mRNA linear EST 19-JAN-2001
LOCUS nab43b10.x1 Soares NSF P8 9W OT PA P S1 Homo sapiens cDNA clone
DEFINITION IMAGE:3268555 3' similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ;
mRNA sequence.

ACCESSION BP435134
VERSION BP435134
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 452.

FEATURES
SOURCE

Location/Qualifiers
1..512
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3268555"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HP8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 512;
Best Local Similarity 95.6%; Pred. No. 3.1e-71;
Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACACCTCAGATTCCA 60
DB 186 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACACCTCAGATTCCA 245
QY 61 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 246 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 305
QY 121 GTTGTGACAAAAGACACTTATCTATGAAGAGTCTTTTATCTTGGCAGATAT 180
DB 306 GTTGTGACAAAAGACACTTATCTATGAAGAGTCTTTTATCTTGGCAGATAT 365
QY 181 ATTATGACTAAGCATTTATGATGAGAGCAACATATTGTATTTGTTCAATGAT 240
DB 366 ATTATGACTAAGCATTTATGATGAGAGCAACATATTGTATTTGTTCAATGAT 425
QY 241 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGAGCAGAGAAAATATAT 300
DB 426 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGAGCAGAGTAATCTTC 485
QY 301 ACCATGATCTACAGGAA 317
DB 486 AGTTAGTCCATTGTAA 502

Search completed: October 18, 2004, 14:51:57
Job time : 7339 secs

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